

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:07 ; Search time 19.66 Seconds

(without alignments)
1055.712 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIVHTKEVKEVA.....LRVNOTFNMNTTKQEHPPDN 216

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	2 A45803	B-cell-restricted
2	1085	94.4	289	2 G00031	B7 protein - red-c
3	738	64.2	299	2 I46680	CD80 precursor - r
4	601.5	52.3	321	2 I54766	B-lymphocyte activ
5	561	48.8	309	2 I49503	CD86 spliced varia
6	185	16.1	275	2 JC7604	B7-2 antigen - hum
7	182	15.8	329	1 A48754	gene B7-2 protein
8	152	13.2	309	2 I49522	CD86 precursor - r
9	140.5	12.2	330	2 I46691	alcam - human
10	133.5	11.6	583	2 I39438	BATF1 protein
11	129	11.2	221	1 Q08E48	butyrophilin precu
12	127	11.1	526	2 S70587	adhesion molecule
13	122.5	10.7	588	2 JH0506	surface glycoprote
14	122.5	10.7	588	2 A45254	SHP substrate-1 pr
15	120.5	10.5	509	2 JC5288	SHP substrate-1 pr
16	120.5	10.5	513	2 JC5289	butyrophilin - mou
17	118	10.3	487	2 S65133	neural cell adhesi
18	116.5	10.1	1088	1 IUXLNL	neural cell adhesi
19	115	10.0	761	1 JH0HNG	neural cell adhesi
20	112.5	9.8	725	2 JH0039	neural cell adhesi
21	110.5	9.6	587	2 JH0464	DM-GRAP precursor
22	109.5	9.5	646	2 I38049	cell surface glyco
23	109.5	9.5	853	2 I38049	neural cell adhesi
24	109	9.5	526	2 A37821	butyrophilin - bov
25	109	9.5	2029	1 TDFELK	protein-tyrosine-p
26	108	9.4	871	1 I48696	protein-tyrosine k
27	108	9.4	881	1 I48697	protein-tyrosine k
28	107.5	9.4	5175	2 T30992	hypothetical prote
29	107.5	9.4	5198	2 T43290	hemiscentin precurs

ALIGNMENTS

30	106.5	9.3	333	2 A31923	amalgam protein pr
31	106.5	9.3	858	1 IJRTNC	neural cell adhesi
32	106	9.2	267	2 PL0064	T-cell receptor be
33	105.5	9.2	1091	1 IJCHNL	neural cell adhesi
34	104.5	9.1	210	2 A56169	Ig kappa chain V r
35	104	9.1	307	1 R4MSBC	T-cell receptor be
36	104	9.1	725	2 JE0100	neural cell adhesi
37	104	9.1	1092	2 JH0635	neural cell adhesi
38	103.5	9.0	480	2 A56182	fibroblast growth
39	103.5	9.0	725	1 IJMSNG	neural cell adhesi
40	103.5	9.0	1115	1 IJMSNL	neural cell adhesi
41	103	9.0	423	2 T29549	hypothetical prote
42	103	9.0	1273	2 T42405	sax-3 protein - Ca
43	102.5	8.9	503	2 JC5287	SHP substrate-1 pr
44	102	8.9	1443	2 I50600	neogenin - chicken
45	101	8.8	1033	2 S19247	cell adhesion prot

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human

N:Alternate names: B-lymphocyte activation antigen B7

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C:Accession: I54495; A45803

R:Selvakumar, A.; Mohanraj, B.R.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

Immunogenetics 36, 175-181, 1992

A:Title: Genomic organization and chromosomal location of the human gene encoding the

A:Reference number: I54495; MUID:92307753

A:Accession: I54495

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: GB:M83077; NID:q179327; PIDN:AAA58390.1; PID:q179329

R:Freeman, G.J.; Freedman, A.S.; Segall, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

J. Immunol. 143, 2714-2722, 1989

A:Title: B7, a new member of the Ig superfamily with unique expression on activated a

A:Reference number: A45803; MUID:90010147

A:Accession: A45803

A:Molecule type: mRNA

A:Residues: 1-288 <FRS>

A:Cross-references: GB:M27533; NID:q184680; PIDN:AAA36045.1; PID:q306916

A:Genetics: CD80; CD28LG1; CD28

A:Cross-references: GDB:251792; OMIM:112203

A:Map position: 3q13.3-3q21

A:Introns: 34/1; 140/1; 234/1; 266/1

C:Keywords: B-lymphocyte restricted antigen B7

C:Keywords: transmembrane protein

F:1-6/Domain: signal sequence #status predicted <SIG>

F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 2,1e-85;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHFCSGVIVHTKEVATLSCGHNVSELAQRIYVOKKKWVLTMSGDMNIATPE	60
DB	27	GLSHFCSGVIVHTKEVATLSCGHNVSELAQRIYVOKKKWVLTMSGDMNIATPE	86
QY	61	YKNTITFDITNNLSIVTLALRPSDEGTCVYLKYEKDAFKREHLAEVTLVYKADPTPS	120
DB	87	YKNTITFDITNNLSIVTLALRPSDEGTCVYLKYEKDAFKREHLAEVTLVYKADPTPS	146
QY	121	ISDFEIPTSNIRITICSTGSGPPEPHLSWLENGEELNATNTVVSOPPEIYAVSSKIDP	180
DB	147	ISDFEIPTSNIRITICSTGSGPPEPHLSWLENGEELNATNTVVSOPPEIYAVSSKIDP	206
QY	181	NMTNHSFMCILIKYGLLRVNOTFNMNTTKQEHPPDN	216

Db 207 NMTHNSFMCLIKYGHRLVNOTFNMNTKOEHPDN 242

RESULT 2

B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031

R:Villinger, F.J.

submitted to the EMBL Data Library, January 1995

A:Reference number: G00217

A:Accession: G00031

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-289 <VIL>

A:Cross-references: EMBL:U019833; NID:9644783; PIDN:AAA86700.1; PID:9644784

A:Genetics:

A:Gene: B7

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match

Best Local Similarity 94.4%; Score 1085; DB 2; Length 289;

Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVHYTEKEKVAATLSCGHNVSEELAQTRITYWQEKKAVLTMGSDMNIMPEY 61

Db 28 LSHFCSGVHYTEKEKVAATLSCGHNVSEELAQTRITYWQEKKAVLTMGSDMNIMPEY 87

QY 62 KNRIPTDITNNLSVIALRPSDEGTVECVLKEKDAFKREHLAEVTLVSKADFPPTSI 121

Db 88 KNRIPTDITNNLSVIALRPSDEGTVECVLKEKDAFKREHLAEVTLVSKADFPPTSI 147

QY 122 SDEIPTSNIRIRICSTSGGFPPEHLISWLENGEELNAINTVSODPETELVAVSSKIDFN 181

Db 148 TDEIIPSPNIRIRICSTSGGFPPEHLISWLENGEELNAINTVSODPETELVAVSSKIDFN 207

QY 182 MTNNHSPMCLIKYGHRLVNOTFNMNTKOEHPDN 216

Db 208 MTNNHSPMCLIKYGHRLVNOTFNMNTKOEHPDN 242

RESULT 3

146690

CD80 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999

C:Accession: I46690

R:Isono, T.; Seto, A.

Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule

A:Reference number: I46689; MUID:95369849

A:Accession: I46690

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-299 <ISO>

A:Cross-references: GB:I49843; NID:9755096; PIDN:BA08643.1; PID:9755097

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match

Best Local Similarity 64.2%; Score 738; DB 2; Length 299;

Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HRCSGVIHTYKEKVAATLSCGHNVSEELAQTRITYWQEKKAVLTMGSDMNIMPEYKN 63

Db 29 HRCSGVIHTYKEKVAATLSCGHNVSEELAQTRITYWQEKKAVLTMGSDMNIMPEYKN 88

QY 64 RTTFDITNNLSVIALRPSDEGTVECVLKEKDAFKREHLAEVTLVSKADFPPTSI 123

Db 89 RTTFDITNNLSVIALRPSDEGTVECVLKEKDAFKREHLAEVTLVSKADFPPTSI 148

QY 124 FEIPTSNIIRICSTSGGFPPEHLISWLENGEELNAINTVSODPETELVAVSSKIDFNMT 183

Db 149 IGHPDPNKRIRICSGGFPPEHLISWLENGEELNAINTVSODPETELVAVSSKIDFNMT 208

QY 184 TNHSPMCLIKYGHRLVNOTFNMNTKOE 211

Db 209 NNHSIVCLIKYGHRLVNOTFNMNTKOE 236

RESULT 4

154766

B-lymphocyte activation antigen 7-1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000

C:Accession: I54766

R:JUDGE, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turkka, L.A.

Int. Immunol. 7, 171-178, 1995

A:Title: Cloning the rat homolog of the CD28/CTLA-4 ligand B7-1: structural and funct

A:Reference number: I54766; MUID:95252184

A:Accession: I54766

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-321 <RES>

A:Cross-references: EMBL:U05593; NID:9453381; PIDN:AAA80154.1; PID:9453382

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match

Best Local Similarity 52.3%; Score 601.5; DB 2; Length 321;

Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY 1 GLSHFCSGVHYTEKEKVAATLSCGHNVSEELAQTRITYWQEKKAVLTMGSDMNIMPEY 59

Db 31 GLDQSSGIVGVQSVKREKALLSCDYKFCSEBSHRIITWQKIDKNVLSVTSVPEVWP 90

QY 60 EYKRTIFDITNNLSVIALRPSDEGTVECVLKEKDAFKREHLAEVTLVSKADFPPT 119

Db 91 KYKRTIYDIAANNYSFSLGLISDRGTTCVQVQREYGGSVYKHLITVELSVADPPT 150

QY 120 SISDEIPTSNIRIRICSTSGGFPPEHLISWLENGEELNAINTVSODPETELVAVSSKID 179

Db 151 NITEYGNPSADIKRITCFASGGFPKPRLSWLENGREELNGINTTISODPESLTYTSOLD 210

QY 180 FNMTHNSFMCLIKYGHRLVNOTFNM 205

Db 211 FNATYDHFIDCFIEYGDVAHVSONFTW 236

RESULT 5

149503

B-lymphocyte activation antigen 7 precursor - mouse

N:Alternate names: MB7-2

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C:Accession: I49503; S17291; I49521

R:Selvakumar, A.; White, P.C.; Dupont, B.

Immunogenetics 38, 292-295, 1993

A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.

A:Reference number: I49503; MUID:93307789

A:Accession: I49503

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-309 <RES>

A:Cross-references: GB:I12589; NID:9293299; PIDN:AAA37240.1; PID:9293301

J. Freeman, G.J.; Gray, G.S.; Gimpl, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge

J. Exp. Med. 174, 625-631, 1991

A:Title: Structure, expression, and T cell costimulatory activity of the murine homol

A:Reference number: S17291; MUID:91341422

A:Accession: S17291

A:Molecule type: mRNA

A:Residues: 1-274, 'R', 279-309 <PRE>

A:Cross-references: EMBL:X60958; NID:950111; PIDN:CAA43291.1; PID:950112

Biochim. Biophys. Acta 1306, 1-4, 1996
 A:Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor
 A:Reference number: S70587; MUID:96201696
 A:Accession: S70587
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-526 <TRAY>
 A:Cross-references: EMBL:U09576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

Query Match 11.1%; Score 127; DB 2; Length 526;
 Best Local Similarity 27.5%; Pred. No. 0.014;
 Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSEELAQTRIVQKKEKMYLTFMMSG---DMNIWPEKKNRTIP--- 67
 DB 42 VGDADLPCLPCLSPNASEHL-ELRMFRKKVSPAVLVHRODRQDEAEQMPYRGRATLYOD 100
 QY 68 -DITNNLSIVIALRPSDEGTVCVYLKYEKDAFKREHLAEVTLVSKADFPSPISDFEI 126
 DB 101 GJAKGVAVLRIRGVRSVSDGEYTCF--FREDGSEYEL--VHLKVALGSDPHIS-MQY 154
 QY 127 PYSNIRITCSTSGGPEPHLSW-LENGEELNINTVSODPETE-LYAVSSKIDFMTT 164
 DB 155 QENGEICLECTSGVTPPEPOVWRTSKGEKFP--STSESNPDEGLETFVAASVILRTDS 212
 QY 185 NMSFMCILIK 193
 DB 213 TKNVSCYIQ 221

RESULT 13
 JH0506
 adhesion molecule SC1 precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
 C:Accession: JH0506; PS0270
 R:Itanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.; Neuron 7, 535-545, 1991
 A:Title: Molecular cloning and expression of a novel adhesion molecule, SC1.
 A:Reference number: JH0506; MUID:92030150
 A:Accession: JH0506
 A:Molecule type: mRNA
 A:Residues: 1-588 <TAN>
 A:Cross-references: GB:S63276; NID:9238000; PIDN:AAB20170.1; PID:9238001
 A:Experimental source: embryo
 A:Accession: PS0270
 A:Molecule type: protein
 A:Residues: 34-48 <TAN>
 C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
 C:Keywords: glycoprotein; transmembrane protein
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-588/Product: adhesion molecule SC1 #status predicted <ADH>
 F:500-523/Domain: transmembrane #status predicted <TRA>
 F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 10.7%; Score 122.5; DB 2; Length 588;
 Best Local Similarity 25.7%; Pred. No. 0.036;
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEKKNRTIFDITNNLSIVIALRPSDEGTVCVYLKYEKDAFKREHLAEVTLVSKADFPPT 118
 DB 90 PDKKDR-LSLSENVTLISIKNARISDEKRFVCLVT-EDDVSEEPYVVKV-----FKQ 139
 QY 119 PS-----ISDFEIPSNIRI-ICSTSGGPEPHLSWLENG-----EELNAINITVSQ 165
 DB 140 PPOPELLHQADF-LETEKLMKLGECVVRDSYPEGNVTWTKNGVLOPVEEVVYINLRKYE 198
 QY 166 DPETELVAVSSKIDFNMNT---TNHSFMCILIKY 194
 DB 199 NRSTGLFTMTSSIQWMPTEKEDANAKFTCIYTY 230

RESULT 14
 A45254
 surface glycoprotein BEN precursor - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
 C:Accession: A45254; S19202
 R:Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.
 Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
 A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed

A:Reference number: A45254; MUID:92302224
 A:Accession: A45254
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-588 <POU>
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088
 C:Keywords: glycoprotein

Query Match 10.7%; Score 122.5; DB 2; Length 588;
 Best Local Similarity 25.7%; Pred. No. 0.036;
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEKKNRTIFDITNNLSIVIALRPSDEGTVCVYLKYEKDAFKREHLAEVTLVSKADFPPT 118
 DB 90 PDYKDR-LSLSENVTLISIKNARISDEKRFVCLVT-EDDVSEEPYVVKV-----FKQ 139
 QY 119 PS-----ISDFEIPSNIRI-ICSTSGGPEPHLSWLENG-----EELNAINITVSQ 165
 DB 140 PPOPELLHQADF-LETEKLMKLGECVVRDSYPEGNVTWTKNGVLOPVEEVVYINLRKYE 198
 QY 166 DPETELVAVSSKIDFNMNT---TNHSFMCILIKY 194
 DB 199 NRSTGLFTMTSSIQWMPTEKEDANAKFTCIYTY 230

RESULT 15
 JCS288
 SHP substrate-1 protein, 509 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
 C:Accession: JCS288
 R:Itanaka, H.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioaka, Biochim. Biophys. Res. Commun. 231, 61-67, 1997
 A:Title: Mouse and human SHP-1: Molecular cloning of cDNAs and chromosomal localization
 A:Reference number: JCS287; MUID:97223399
 A:Contents: Brain
 A:Accession: JCS288
 A:Molecule type: mRNA
 A:Residues: 1-509 <YAM>
 A:Cross-references: DBJ:D87967; NID:q1864012; PIDN:BAAL3520.1; PID:q1864013
 C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c acts as a docking protein and induce translocation of SHP-2 from the cytosol to the
 C:Genetics:
 A:gene: shps-1
 A:Map position: 2

Query Match 10.5%; Score 120.5; DB 2; Length 509;
 Best Local Similarity 25.9%; Pred. No. 0.044;
 Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

QY 3 SHPCSGV---IHVTRKEVEA-----TLSCGHNVSEELAQTRIVQK---EKKMYL 48
 DB 23 SCFTGVGTGKELKLVTPDEKSVSAAGSYVLNC---TIVSLVGVPIKWRGVGQSLIL 79
 QY 49 TNMSGDMNTPPEKKNRTIFDIT---NNL--STVIALRPSDEGTVCVYLKYEKDAFKREH 104
 DB 80 YSFTGEH--FPRVTN--VSDATKRNMDSEIRISNTPPEAGTYVCV--KFGQSPSPDPPT 133
 QY 105 L-----AEVTLVSKADFPPT--ISDFEIPSNIRIICSTSGGPEP-HLSWLENGEEL 156
 DB 134 EIOGGGTEVYVLAKPSPPEVSGPADRGIDPKV-NFTCKSHGSPRNITLKWFKDGOEL 192

Tue Jun 18 11:51:13 2002

us-09-454-651b-23.rpr

Page 6

```
Qy      157 NAINTVSODETELEYAVSS--KIDENNTTHSEKLICKYHLRNQT 202  
        : : ||| : | :|| :: | || : : : :  
Db      193 HHLETTNPSGRKNVSYNSTPVRVLNSMDVHS-KVICEVAHITLDRS 239
```

Search completed: June 18, 2002, 11:43:56
Job time: 49 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:57 ; Search time 11.96 Seconds
(without alignments)
699.283 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149
Sequence: 1 GLSHFGSGVHTVKEKFEVA.....LRVNOTFNMTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	1 CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1 CD80_RABIT	P42070 oryctolagus
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculu
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1 ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculu
7	150.5	13.1	322	1 ICOL_MOUSE	O91h18 mus musculu
8	140.5	12.2	330	1 CD86_RABIT	P42071 oryctolagus
9	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculu
10	133.5	11.6	583	1 C166_HUMAN	O13740 homo sapien
11	129	11.2	221	1 BRF1_EBV	P03228 Epstein-Bar
12	127	11.1	526	1 BUTY_HUMAN	Q13410 homo sapien
13	122.5	10.7	588	1 C166_CHICK	P42292 gallus gall
14	119	10.4	524	1 BUTY_MOUSE	O62556 mus musculu
15	116.5	10.1	1088	1 NCAL_XENLA	P16170 xenopus lae
16	115	10.0	761	1 NCAL_HUMAN	P13592 homo sapien
17	115	10.0	848	1 NCAL_MOUSE	P13591 homo sapien
18	110.5	9.6	321	1 TCB_ELV	P43121 feline leuk
19	109.5	9.5	646	1 M018_HUMAN	P11364 feline leuk
20	109.5	9.5	853	1 NCAL_BOVIN	P31836 bos taurus
21	109	9.5	526	1 BUTY_BOVIN	P18892 bos taurus
22	109	9.5	2029	1 LAR_DROME	P16621 drosophila
23	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculu
24	107.5	9.4	333	1 AMAL_DROME	P13564 drosophila
25	106.5	9.3	858	1 NCAL_RAT	P13596 rattus norv
26	105	9.1	319	1 A33_HUMAN	O99795 homo sapien
27	105	9.1	1091	1 NCAL_CHICK	P33590 gallus gall
28	104	9.1	1092	1 NCAL_XENLA	P36335 xenopus lae
29	103.5	9.0	725	1 NCAL_MOUSE	P13594 mus musculu
30	103.5	9.0	1115	1 NCAL_MOUSE	P13595 mus musculu
31	103	9.0	298	1 JN42_HUMAN	P57087 homo sapien
32	102	8.9	1443	1 NCAL_CHICK	O90610 gallus gall
33	101.5	8.8	403	1 RAGE_MOUSE	O62151 mus musculu

34	100	8.7	413	1 HEMO_MANSE	P31398 manduca sex
35	99.5	8.7	1338	1 VGR1_HUMAN	P17948 homo sapien
36	98.5	8.6	365	1 CXAR_HUMAN	P78310 homo sapien
37	98.5	8.5	278	1 OX2G_RAT	P04218 rattus norv
38	98	8.5	298	1 JAM1_BOVIN	O91t56 bos taurus
39	98	8.5	1333	1 VGR1_MOUSE	P35969 mus musculu
40	97	8.4	1336	1 VGR1_RAT	P53767 rattus norv
41	96.5	8.4	739	1 VCA1_HUMAN	P19320 homo sapien
42	96	8.4	1020	1 CONT_MOUSE	P12960 mus musculu
43	95.5	8.3	811	1 FS22_DROME	P34083 drosophila
44	95.5	8.3	873	1 FS21_DROME	P34082 drosophila
45	95.5	8.3	1348	1 VGR2_CORVA	P52583 coturnix co

ALIGNMENTS

RESULT 1
CD80_HUMAN STANDARD: PRT: 288 AA.
ID CD80_HUMAN
AC P33681;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=90010147; PubMed=2794510;
RA Nadler L.M.;
RA Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RT "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells."
RL J. Immunol. 143:2714-2722(1989).
[2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307753; PubMed=1377173;
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RT Dupont B.;
RL "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."
RL Immunogenetics 36:175-181(1992).
[3]
RN [4]
RP SEQUENCE OF 35-38.
RX MEDLINE=91341422; PubMed=1714935;
RA Freeman G.J., Gray G.S., Gimm C.D., Lombard D.B., Zhou L.-J.,
RA White M., Fingerhuth J.D., Gibben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7."
RL J. Exp. Med. 174:625-631(1991).
[4]
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=95084403; PubMed=7527824;
RA Lantier L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."
RL J. Immunol. 154:97-105(1995).
[5]
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX MEDLINE=20125021; PubMed=10661405;
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA Jones E.Y., Stuart D.I., Davis S.O.;
RT "Structure and dimerization of a soluble form of B7-1."
RL Immunity 12:51-60(2000).
[6]
RN [7]
RP FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
CC AND DENDRITIC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- DATABASE: NAME-PROV; NOTE-CD guide CD80 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M21533; AAA36045.1; -;
DR EMBL; M83077; AAA58390.1; -;
DR EMBL; M83072; AAA58390.1; JOINED.
DR EMBL; M83073; AAA58390.1; JOINED.
DR EMBL; M83074; AAA58390.1; JOINED.
DR PIR; A45803; A45803
DR PIR; I489; 10-JAN-01.
DR MIM; I12203; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 288 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 35 242 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 243 263 POTENTIAL.
FT DOMAIN 264 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 123 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 155 223 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 50 116
FT DISULFID 162 216
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 288 AA; 33048 MW; BA453EE34528B1F4 CRC64;

Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.5e-89;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 207 NMTNHSFCLIKYGLHVRNQTFFNMTTKQEHFPD 242
RESULT 2
ID CD80_RABIT STANDARD; PRT; 299 AA.
AC P42070;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen).
GN CD80.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B/J X CHB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D49843; BAA08643.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 32
FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 115
FT DISULFID 161 215
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 299 AA; 33513 MW; 6744223E5CC91DE0 CRC64;

Query Match 64.2%; Score 738; DB 1; Length 299;
Best Local Similarity 63.9%; Pred. No. 8.9e-55;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

[illegible]

Query Match	48.8%;	Score 561;	DB 1;	Length 306;
Best Local Similarity	50.7%;	Pred. No. 5.9e-40;		
Matches 104;	Conservative 41;	Mismatches 58;	Indels 2;	Gaps
DR EMBL: L12589; AAA37240.1; ALT_SEQ.				
DR EMBL: L12585; AAA37240.1; JOINED.				
DR EMBL: L12586; AAA37240.1; JOINED.				
DR EMBL: L12587; AAA37240.1; JOINED.				
DR EMBL: L12588; AAA37240.1; JOINED.				
DR PIR: S17291; S17291.				
DR MGD: MGI:101775; CD80.				
DR InterPro: IPR003599; Ig.				
DR InterPro: IPR003006; Ig_MHC.				
DR InterPro: IPR003600; Ig_Like.				
DR Pfam: PF00047; Ig; 2.				
DR SMART: SM00409; Ig; 1.				
DR SMART: SM00410; Ig_Like; 1.				
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.				
FT SIGNAL 1 37				
FT CHAIN 38 306				
FT DOMAIN 38 246				
FT TRANSMEM 247 268				
FT DOMAIN 269 306				
FT DOMAIN 47 126				
FT DOMAIN 158 226				
FT DOMAIN 227 246				
FT DISULFD 54 119				
FT DISULFD 165 219				
FT CARBOHD 93 93				
FT CARBOHD 99 99				
FT CARBOHD 149 149				
FT CARBOHD 189 189				
FT CARBOHD 210 210				
FT CARBOHD 214 214				
SQ SEQUENCE 306 AA; 34589 MM; 1DBADE0931B84C62 CRC64;				
Query Match	48.8%;	Score 561;	DB 1;	Length 306;
Best Local Similarity	50.7%;	Pred. No. 5.9e-40;		
Matches 104;	Conservative 41;	Mismatches 58;	Indels 2;	Gaps
QY 12 VTKEVEKVAATISCGHNVSVELAQTRIYQKKEKKMVLTMNSGDMNIMPEKNTIDITN 71				
DB 42 ISKSKYKDVLLPCRRNSDHEDESEDRITYQMCHDVLVSLVIAKTKVMEPKNRLDYNT- 100				
QY 72 NLSIYILALRPDEETGYCVLYLTKEDAFKREHLAEVTLISKVADPPPSISDEEIPSTN 131				
DB 101 TYSLITLLIGLVLSDRKTYSCVQKKEKRGIEYKHLALYKLSKADFPSPNTESQNPADT 160				
QY 132 RRIICSTSGGPEPHLSWLENGEELINATNTVSODPETELAYVASKIDFNKNTNHSFCL 191				
DB 161 KRITCFASGFPKPRFSLWMLGRELPGINTIISODPESELYTIISSQIDFNTNRHTIKCL 220				
QY 192 IKYGHLYRNQFFNMNTTKQEHPPDN 216				
DB 221 IKYGDHVSDEFTWEKPPEDP-PDS 244				
RESULT 4				
CD86_HUMAN	STANDARD;	PRT;	329 AA.	
AC P42081; Q13655;				
DT 01-NOV-1995 (rel. 32, Created)				
DT 01-NOV-1995 (rel. 32, Last sequence update)				
DT 01-MAR-2002 (rel. 41, Last annotation update)				
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (F0N-1) (BU63).				
DE CD86 OR CD86G2.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX NCBI_Taxid=9606;				
RN 111				
RP SEQUENCE FROM N.A.				
RX MEDLINE=94053735; PubMed=7694363;				
KA Freeman G.J., Gribben T.G., Boussetis V.A., Ng J.W.,				

RA Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 cell proliferation.";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RL Nadler L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79(1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX TISSUE=FORESKIN;
 RX MEDLINE=9531831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RT "Genomic organization of the gene coding for the costimulatory human
 B-lymphocyte antigen B7-2 (CD86).";
 RL Immunogenetics 42:85-89(1995).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 cell proliferation, cytokine production, and generation of CTL.";
 RL Immunol. 154:97-105(1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Wakasa H., Tedder T.F.;
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and
 activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
 MONOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation-
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L25259; AAA58389.1; -;
 DR EMBL: U04343; AAB03814.1; -;
 DR EMBL: U17722; AAA86473.1; -;
 DR EMBL: U17717; AAA86473.1; JOINED.
 DR EMBL: U17718; AAA86473.1; JOINED.
 DR EMBL: U17719; AAA86473.1; JOINED.
 DR EMBL: U17721; AAA86473.1; JOINED.
 DR MIM: 601020; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.

FT SIGNAL 1 23
 FT CHAIN 24 329
 FT DOMAIN 24 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 329
 FT DOMAIN 33 117
 FT DOMAIN 149 225
 FT DISULFID 40 110
 FT DISULFID 157 218
 FT CARBOHYD 33 33
 FT CARBOHYD 47 47
 FT CARBOHYD 135 135
 FT CARBOHYD 146 146
 FT CARBOHYD 154 154
 FT CARBOHYD 177 177
 FT CARBOHYD 192 192
 FT CARBOHYD 213 213
 FT CONFLICT 27 27
 SQ SEQUENCE 329 AA; 37696 MW; 65d4f3826899c7fd CRC64;
 Query Match 15.8%; Score 182; DB 1; Length 329;
 Best Local Similarity 29.0%; Pred. No. 3.3e-08;
 Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;
 QY 18 EVATLSC---GHNVSVELAQTIRYQKRMVLTMM---SGDMNIMPEYKNTPTDI 69
 DB 34 ETADLPQCFANSQNSQSELY---VFWDQDENLVINEVLYLQKKEKFDVSHSKYMRISD- 89
 QY 70 TNNISVTLALRPDEGVEVLYEKDAKREHLAEVLSKADPEPTSPISDPEIPTS 129
 DB 90 SDSVTLRLHNIQIKDKYQCIHHKKPTGMIRHONNSELVLANSQPEI---VPIS 145
 QY 130 NIR-----RIICSTSGGPEP-HLSWLENGEELNAINTV-----SDDPEIYAYS 175
 DB 146 NITENVYINILTCSSIHGPEPKMSV-----LTKNSTIERYDGIKMSQDNVTELDVS 200
 QY 176 SKLDF---NMTNHSFMCILKYGLHY 199
 DB 201 ISLSVSEPDVSNMTIFCIETEDTKRTL 227
 RESULT 5
 ICOL_HUMAN STANDARD; PRT; 302 AA.
 AC 075144; Q9NRQ1; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GL50)
 DE (B7-related protein-1) (B7RP-1).
 GN ICOSL OR B7H2 OR B7RP1 OR KIA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell.
 RX MEDLINE=20477846; PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 ICOS.";
 RL Blood 96:2808-2813(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20465019; PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
 RT "Characterization of a new human B7-related protein: B7RP-1 is the
 ligand to the co-stimulatory protein ICOS.";

RL Int. Immunol. 12:1439-1447(2000).

RM [3] SEQUENCE FROM N.A. (ISOFORM 2).

RN TISSUE=Leukocyte;

RC MEDLINE=20126021; PubMed=10657606;

RA Ling V., Wu P.W., Finnelly H.F., Bean K.M., Spaulding V., Fouser L.A.,

RT Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,

RT Jacobs K.A., Collins M.;

RT "Identification of GL50, a novel B7-like protein that functionally

RT binds to ICOS receptor.";

RT J. Immunol. 164:1653-1657(2000).

RL [4]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RK MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RT Kohani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.";

RL DNA Res. 5:169-176(1998).

RN [5]

RA SEQUENCE FROM N.A. (ISOFORM 2).

RL Ling V., Dunussi-Joannopoulos K.;

RT "GL50 molecules and uses therefor.";

RT Patent number WO0121796, 29-MAR-2001.

CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR

CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND

CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND

CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN

CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS

CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-

CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2;

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,

CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE

CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,

CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN

CC LYMPH NODES, LEUKOCYTES AND SPLEEN.

CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY

CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND

CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG

CC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300

CC onward for an unknown reason.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL; AF199028; AAF34739.1; -

DR EMBL; AF289028; AAG01176.1; -

DR EMBL; AF216749; AAK16241.1; -

DR EMBL; AB014553; BAA1628.1; ALT-SEQ.

DR EMBL; AX100595; CAC36465.1; -

DR MIM; 605717; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003600; Ig_Like.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00409; Ig_1.

DR SMART; SM00410; Ig_Like; 1.

DR B-cell activation; Immune response; Glycoprotein;

DR Immunoglobulin domain; Signal; Transmembrane; Multigene family;

KW

KW Alternative splicing.

FT SIGNAL 1 18

FT CHAIN 19 302

FT DOMAIN 19 256

FT TRANSMEM 257 277

FT DOMAIN 278 302

FT DOMAIN 30 120

FT DOMAIN 151 223

FT DISULFID 37 113

FT DISULFID 158 216

FT CARBOHYD 70 70

FT CARBOHYD 137 137

FT CARBOHYD 173 173

FT CARBOHYD 186 186

FT CARBOHYD 225 225

FT VARSPLIC 300 302

FT SEQUENCE 302 AA; 33349 MW; 647934E21B55E34A CRC64;

Query Match 14.0%; Score 161; DB 1; Length 302;

Best local Similarity 26.4%; Pred. No. 1,7e-06;

Matches 57; Conservative 36; Mismatches 95; Indels 28; Gaps 8;

QY 14 KEYKEY-----ATLSCG-HNVSVEELAQTRIYQ-KERKMYLT-----MMSGDNIMPEYKN 63

DB 23 KEVRAMVGSDELSCACPEGRFDLDVYVYVQTSKVTYTHIPONSLENDVDSRYRN 82

QY 64 RTTFD-----ITNNLSVILLALRSDSGTECVLKEKDAFKREHAEVTLKAPFP 119

DB 83 RAMSPAGMIRGFSRLNVPVPODEQKFCVLVS-OSLGFQEVLSVEVTLHVAANFSVP 141

QY 120 SISDFEIPTSNIRRICSTSGGPEPHLSLWENGELNINFTVSODPETE-----L 171

DB 142 VVSAPHSPODELTFCTCSINGPRNVYWKNTD-----NSLLDQALQNDYFLNMRGL 196

QY 172 YAVSKLDNFMNTTMSFMCILIKYGHILRVNQTENWNT 207

DB 197 YDVSVYLRIARPTSPVNGICIEENVLLQNLIVGSGQT 232

RESULT 6

CD86_MOUSE STANDARD; PRT; 309 AA.

AC P42082;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE T lymphocyte activation antigen CD86 precursor (Activation B7-2

DE antigen) (Early T cell costimulatory molecule-1) (ETC-1).

GN CD86.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RK MEDLINE=94065585; PubMed=7504059;

RA Freeman G.J., Borriello F., Hodes R.J., Relser H., Gribben J.G.,

RA Wang S., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,

RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates

RT T cell proliferation and interleukin 2 production.";

RL J. Exp. Med. 178:2185-2192(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129;

RK MEDLINE=96094437; PubMed=7499829;

RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;

RT "Differential expression of alternate mB7-2 transcripts.";

RL J. Immunol. 155:5490-5497(1995).

RN [3]

RP SEQUENCE OF 7-309 FROM N.A.

RK MEDLINE=94230971; PubMed=7513726;

RA	Chen C., Gault A., Shen L., Nabavi N.;
RT	"Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule.";
RL	J. Immunol. 152:4929-4936(1994).
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on how it can be used by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announcement/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L25606; AAA79770.1; -
DR	EMBL; U39456; AAC52334.1; - JOINED.
DR	EMBL; U39459; AAC52334.1; JOINED.
DR	EMBL; U39461; AAC52334.1; JOINED.
DR	EMBL; U39462; AAC52334.1; JOINED.
DR	EMBL; U39463; AAC52334.1; JOINED.
DR	EMBL; U39464; AAC52334.1; JOINED.
DR	EMBL; U39465; AAC52334.1; JOINED.
DR	EMBL; U39466; AAC52334.1; JOINED.
DR	EMBL; U39456; AAC52336.1; AL1_INIT.
DR	EMBL; U39461; AAC52336.1; JOINED.
DR	EMBL; U39462; AAC52336.1; JOINED.
DR	EMBL; U39463; AAC52336.1; JOINED.
DR	EMBL; U39464; AAC52336.1; JOINED.
DR	EMBL; U39465; AAC52336.1; JOINED.
DR	EMBL; U39466; AAC52336.1; JOINED.
DR	MGI; MGI:101773; Cd86.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	SMART: SMO0406; IGV: 1.
DR	PROSITE; PS00290; IG_MHC; FALSE_NRG.
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.
FT	SIGNAL 1 23 POTENTIAL.
FT	CHAIN 24 309 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT	DOMAIN 24 244 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 245 265 POTENTIAL.
FT	DOMAIN 266 309 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT	DOMAIN 149 223 IG-LIKE C2-TYPE DOMAIN.
FT	DISELFED 40 110 POTENTIAL.
FT	DISULFED 157 216 POTENTIAL.
FT	CARBOHD 33 33 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 47 47 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 92 92 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 135 135 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 146 146 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 154 154 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 175 175 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 190 190 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHD 231 231 N-LINKED (GLCNAC . .) (POTENTIAL).
SEQ	SEQUENCE 309 AA: 34665 MW: 8558DCD1B81D5EA CRC64:

Query Match	13.28;	Score 152;	DB 1;	Length 309;
Best Local Similarity	26.18;	Pred. No. 9.9e-06;		
Matches	52;	Conservative	43;	Mismatches 78;
				Indels 26;
				Gaps 10

Oy	20	ATLSC----	GNHVSVEELAQRIRYQKCKMVL-----TWMSGDMNIMPEYKRRITFDI	69
Db	36	AYLPPEPTKAONISISELV--	VWDDQKQIVLEHNLIGTFKLDVN--AKYIGRTSFD-	89
Oy	70	TNNLSIVTLARPSPDEGT	ECVLEKYEK--DAFKREHLAEVTLISVKADEPTPSISDEIP	127
Db	90	RNNMTLRHLHNVQIKDMGSD	FDICFKPPGTSIILOQTLE--LSVIANFSEPEIKLAQNV	147
Oy	128	TSNIR-RICGTS	SGGFPEPHLSW--LENGELNAINTVSGDPETELXAVSKIDFNM--	187
Db	148	TGNSGINSITCTSKQGHPPK	KMYELFLITNSTNEYGDNMQISODNVTLEFISNLSISLSPD	207
Oy	183	-TTNHSF	MLIKYHRLRYN 200	
Db	208	GWMHTVVCVLETESMKIS	226	
RESULT	7			
ID	ICOL_MOUSE	STANDARD:	PRT:	322 AA.
AC	O9JHJ8:			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	ICOS	ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein g150)		
DE	(B7-related protein-1) (B7RP-1) (LICOS).			
GN	ICOSL OR B7H2 OR B7RP1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.			
RP	TISSUE=Lymphocytes;			
RC	MEDLINE=20083495; PubMed=10617205;			
RA	Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmento U., Guo J.,			
RA	Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tahir-Bilad A.,			
RA	Borankov D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,			
RA	Elliot G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,			
RA	Shaklee C.L., Van G., McCabe T.W., Senaldi G.;			
RT	"T-cell co-stimulation through B7RP-1 and ICOS.";			
RL	Nature 402:827-832(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	TISSUE=Thymus;			
RC	MEDLINE=20015817; PubMed=10549624;			
RA	Swallow M.M., Wallin J.J., Sha W.C.;			
RT	"B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by			
RL	TNFalpha.";			
RT	Immunity 11:423-432(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	STRAIN=C3H/HeJ; TISSUE=Metal thymus;			
RA	MEDLINE=20126021; PubMed=10657606;			
RA	Ling V., Wu P.W., Finerney H.E., Bean K.M., Spaulding V., Fouser L.A.			
RA	Jacobson K.A., Hunter S.E., Zollner R., Thomas J.T., Miyashiro J.S.,			
RA	Leeds J.C., Collins M.;			
RT	"Identification of g150, a novel B7-like protein that functionally			
RT	binds to ICOS receptor.";			
RL	J. Immunol. 164:1653-1657(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RP	TISSUE=Peripheal blood lymphocytes;			
RC	MEDLINE=21286479; PubMed=11390480;			
RA	Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finerney H.F.,			
RA	Collins M.;			
RT	"Differential expression of inducible costimulator-ligand splice			
RT	variants: lymphoid regulation of mouse g150-b and human g150			
RT	molecules.";			
RL	J. Immunol. 166:7300-7308(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			

RA Ling V., Dunussi-Joannopoulos K.,
 RT "G150 molecules and uses thereof."
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION. INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND Peyer's
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYOGENESIS. IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTM/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF216747; AAF45149.1; -
 CC EMBL: AF199027; AAF34738.1; -
 CC EMBL: AX100591; CAC36463.1; -
 CC EMBL: AX100593; CAC36464.1; -
 CC EMBL: AF394451; AAK7544.1; -
 CC MGD: MG1:1354701; Icosl.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003600; Ig_Like.
 CC Pfam: PF00047; Ig_1.
 CC SMART: SM00409; Ig_1.
 CC SMART: SM00410; Ig_Like; 1.
 CC B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing.
 CC FT SIGNAL 1 46
 CC CHAIN 47 322
 CC DOMAIN 47 277
 CC TRANSMEM 278 298
 CC DOMAIN 299 322
 CC DOMAIN 55 145
 CC DOMAIN 178 250
 CC DOMAIN 31 38
 CC DOMAIN 289 292
 CC DOMAIN 62 138
 CC DISULFID 185 243
 CC FT DISULFID 185 243
 CC CARBOHYD 120 71
 CC FT CARBOHYD 120 71
 CC CARBOHYD 163 163
 CC FT CARBOHYD 163 163
 CC CARBOHYD 200 200
 CC FT CARBOHYD 200 200
 CC CARBOHYD 213 213
 CC FT CARBOHYD 213 213
 CC CARBOHYD 252 252
 CC FT CARBOHYD 252 252
 CC CARBOHYD 265 265
 CC FT CARBOHYD 265 265

FT VARSPIC 321 322 HA -> TWAPVQDYLLIPRLYMSPOLKTRGLP (1N
 FT FT ISOFORM 2).
 FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 SQ SEQUENCE 322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;
 Query Match 13.1%; Score 150.5; DB 1; Length 322;
 Best Local Similarity 27.1%; Pred. No. 1,4e-05;
 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;
 QY 2 LSHRC--SGYIHVKEKEVATLSCGHNVS-----ELAQRTIYKOEKKMY-----L 48
 DB 38 LSSICAASETEGAMGWSNVVISC-----IDPRRRFNLISGLVYWOIEPPEVSYYL 92
 QY 49 TMSGDNNIMPEYKRTIFDTN-----NLSTVIALRPDEGTECVLYKEKDAFRRH 104
 DB 93 PYKSPGYNVSSYKRRHLSDSMKGNFSLYKNTVPDQETCYV--FMNATATLYK 150
 QY 105 LAE--VTLVYKADFP--SISDEIPTSNIRITCSGGFPPHLSWLENGEELNAIN 160
 DB 151 ILLEEVRLRVAANSTFVISTDSNPGOE--RTYTCMSKNGYPPNPYWI--NTDNLID 208
 QY 161 TTVSQDP-----ETFLVYVSSKLPFNMTNHSFMCILYGHLRV-----QTFNWTTK 209
 DB 209 TALDNNVYLNKGLDYVITLRLPMTSRGDVLCVENVALHONITSISQASFTGNNTK 268
 RESULT 8
 CD86_RABIT
 ID CD86_RABIT STANDARD; PRT; 330 AA.
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHDB:HM;
 RX MEDLINE=95369849; Pubmed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules."
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D49842; BAA08642.1; -
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003596; Ig_V.
 CC SMART: SM00406; IgV_1.
 CC PROSITE: PS00290; Ig_MHC; 1.


```

RESULT 10
C166_HUMAN
ID C166_HUMAN STANDARD: PRT: 583 AA.
AC 013740; 060892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279947; PubMed=7760007;
RA Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,
RA Wang W.-C., Marguardt H., Neubauer M., Pesando J.M., Francke U.,
RA Haynes B.F., Aruffo A.;
RT "Cloning, mapping, and characterization of activated leukocyte-cell
RT adhesion molecule (ALCAM), a CD6 ligand."
RT J. Exp. Med. 181:2213-2220(1995).
RN [2]
RP SEQUENCE OF 2-583 FROM N.A.
RX MEDLINE=98161527; PubMed=9502422;
RA Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,
RA van Kooyk Y., Bloemers H.P., Swart G.W.;
RT "MEMO, a new cell adhesion molecule in metastasizing human melanoma
RT cell lines, is identical to ALCAM (activated leukocyte cell adhesion
RT molecule).";
RT Am. J. Pathol. 152:805-813(1998).
RN [3]
RP CD6-BINDING DOMAINS.
RX MEDLINE=96420463; PubMed=8823162;
RA Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
RT "Recognition of diverse proteins by members of the immunoglobulin
RT superfamily: delineation of the receptor binding site in the human
RT CD6 ligand ALCAM."
RT Biochemistry 35:12287-12291(1996).
RN [4]
RP 3D-STRUCTURE MODELING OF 28-133.
RX MEDLINE=96060095; PubMed=8520490;
RA Bajorath J., Bowen M.A., Aruffo A.;
RT "Molecular model of the N-terminal receptor-binding domain of the
RT human CD6 ligand ALCAM."
RT Protein Sci. 4:1644-1647(1995).
RN [5]
RP FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
RN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
RN INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
RN ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
RN THE NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD166 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd166.htm".
CC -----
CC this SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L38608; AAB59499.1;
CC EMBL: Y10183; CAA71256.1;
CC PDB: 1KJC; 03-APR-96.
CC MIM: 601662;

```

```

DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00410; Ig_Like; 2.
DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
DR Cell adhesion; Immunoglobulin domain; Transmembrane;
KW Repeat; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 27
FT CHAIN 26 583
FT DOMAIN 28 527
FT TRANSMEM 528 549
FT DOMAIN 550 583
FT DOMAIN 36 120
FT DOMAIN 150 227
FT DOMAIN 263 321
FT DOMAIN 347 399
FT DOMAIN 428 492
FT DISULFID 43 113
FT DISULFID 157 220
FT DISULFID 270 313
FT DISULFID 354 392
FT DISULFID 435 485
FT CARBOHYD 91 91
FT CARBOHYD 95 95
FT CARBOHYD 167 167
FT CARBOHYD 265 265
FT CARBOHYD 306 306
FT CARBOHYD 361 361
FT CARBOHYD 457 457
FT CARBOHYD 480 480
FT CARBOHYD 499 499
FT VARIANT 258 258
FT VARIANT 301 301
FT VARIANT /Frid=VAR_003907.
FT SEQUENCE 583 AA; 65132 MW; E023FB3974A60284 CRC64;
SQ
Query Match 11.6%; Score 133.5; DB 1; Length 583;
Best local similarity 24.5%; Pred. No. 0.00077;
Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;
QY 59 PEYKNTFTDITNNISVIALRPSDEGTVCVVKYKDAFKRHLAEVTLISKADPPT 118
|||:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 84 PEYKDR-LINSEYNTLISNARISDEKRFVCMIVT-EDNVFEAPTIVK-----FKQ 133
QY 119 PSISDFE-----IPSNIRI-ICSTSGFPEPHISWLNGELELAIVTV-----SOD 166
|||:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 134 PSKPEIVSKALFLETQLKKGDCISDSYDGNITWYRNGKVLHPLGAVYIIFKKEMD 193
QY 167 PETELYAVSKIDFNMNT---TNHSPMCLIKY 194
|:|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 194 PVTQLYTMTSTLEYKTKADIQMPFTGSVTV 224
|:|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
RESULT 11
BREF1_EBV STANDARD: PRT: 221 AA.
AC P03228;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 33 kDa early protein (p33).
GN BARE1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_Taxid=10577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;

```

BAER R., Bankier A.T., Biggin M.D., Delinger P.L., Farrell P.J.,
 Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.",
 Nature 310:207-211(1984).
 [2]
 RP IDENTIFICATION OF PROTEIN.
 RX MEDLINE=90059873; PubMed=2555151;
 RA Wei M.X., Ooka T.;
 RT "A transforming function of the BARF1 gene encoded by Epstein-Barr
 virus";
 RL EMBO J. 8:2897-2903(1989).
 CC -1- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V01555; CAA24809.1; -
 DR PIR; A03792; OQBE48.
 DR PIR; S33058; S33058.
 DR InterPro: IPR003600; Ig_Like.
 DR SMART; SM00410; Ig_Like; 1.
 DR Early protein; Oncogene.
 SQ SEQUENCE 221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match 11.2%; Score 129; DB 1; Length 221;
 Best Local Similarity 27.0%; Pred. No. 0.00055;
 Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSEELAQRTIYMOCK-----EKKVYLTMGSGMNIPE 60
 DB 19 QAVTAFLGERVTLIS-----YMRVSLSPREIEVSMFKLGEQGVILGRNHV-IFIE 71
 QY 61 YKRTITDI---TNLSIVIALRPSDEGTVECVLYEKDAFKREHIAEV---TISV-- 112
 DB 72 WPRGEFDHRSANTFELVYTAANISHDGNVLCRMKLGETEVTQKSHLVYKPLTSLVHS 131
 QY 113 -KADFPPTSIDFEIPRTSINRIIRISGSGPPEPHLSML 150
 DB 132 ERSGQF-----DFSVL-----VTCTVNAFPHPHVOWL 159

RESULT 12
 BUTY_HUMAN STANDARD; PRT; 526 AA.
 AC 013410;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Butyrophilin precursor (BT).
 GN BTN1A1 OR BTN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=96201696; PubMed=8611614;
 RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
 RT "Cloning and sequence analysis of human butyrophilin reveals a
 RT potential receptor function.";
 RL Biochim. Biophys. Acta 1306:1-4(1996).
 CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
 CC MAY ACT AS A SPECIFIC MEMBRANE ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE (BY SIMILARITY).

CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
 CC (BY SIMILARITY)
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U39976; AAC50489.1; -
 DR MIM; 601610; -
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003876; SPRY_domain.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00622; SPRY_1.
 DR SMART; SM00406; IgV_1.
 DR SMART; SM00449; SPRY_1.
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 26
 FT CHAIN 1 526
 FT DOMAIN 27 526
 FT TRANSMEM 243 269
 FT DOMAIN 270 526
 FT CARBOHYD 55 55
 FT CARBOHYD 215 215
 SQ SEQUENCE 526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match 11.1%; Score 127; DB 1; Length 526;
 Best Local Similarity 27.5%; Pred. No. 0.0024;
 Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSEELAQRTIYMOCKEKKMVLTMMSG---DMNIPEKKNITP--- 67
 DB 42 VGEPAELPCRLSPASPAEHL-ELRWEKKVSPALVRDGEQDAEQAPPEKRGATLVOD 100
 QY 68 -DITNNLSIVIALRPSDEGTVECVLYEKDAFKREHIAEVTLVAKADFPPTSPISDFEI 126
 DB 101 GIAGKGVALLRIGVRSVDDGEYTCF---FREDGSEEL--VHLKVALGSDPHIS-MQV 154
 QY 127 PITSIRRLICSTSGFPPEPHLSW-LENGEELNAINTVSODPETE-LYAVSSKIDFMNT 184
 DB 155 QENGEILECTSVGWPEPOWRTSKGEKFP--STSESRNPDEEGIFTVAASVYIIRDT 212
 QY 185 NHPFCLIK 193
 DB 213 TKNVSCYIQ 221

RESULT 13
 C166_CHICK STANDARD; PRT; 588 AA.
 AC P42292;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE CD166 antigen precursor (SC1 glycoprotein) (BEN glycoprotein) (DM-
 DE GRASP protein) (Jc7 protein).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN 11)


```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC TISSUE-Embryo:
RX MEDLINE=92030150; PubMed=1931049;
RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RA "Molecular cloning and expression of a novel adhesion molecule, SCL.";
RL Neuron 7:535-545(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=91337449; PubMed=1873027;
RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA Chang S.;
RA "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
RA that supports neurite extension";
RL Neuron 7:209-220(1991).
RN [3]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
RC TISSUE-Bursa of Fabricius;
RX MEDLINE=92302224; PubMed=1608932;
RA Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RA "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
RA expressed in a variety of developing systems.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RN [4]
RN POSSIBLE FUNCTION.
RP MEDLINE=92211411; PubMed=1313497;
RA Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RA "Association of BEN glycoprotein expression with climbing fiber
RA axonogenesis in the avian cerebellum.";
RL J. Neurosci. 12:1548-1557(1992).
RC -1- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOETIC CELLS. EACH
CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC OF BEN.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, S63276; AAB20170.1; -;
DR EMBL, X66678; AAA48602.1; -;
DR EMBL, X64301; CAA45579.1; -;
DR HSSP, Q13740; 1KTC.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; Ig; 3.
DR SMART: SM00410; Ig_Like; 2.
DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 588 CD166 ANTIGEN.
FT DOMAIN 34 532 EXTRACELLULAR (POTENTIAL).
FT TRA5MEM 533 553 POTENTIAL.
FT DOMAIN 554 588 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 126 Ig-Like V-TYPE DOMAIN 1.
FT DOMAIN 156 253 Ig-Like V-TYPE DOMAIN 2.

```

[illegible]


```
FT DOMAIN 149 153 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 158 162 HEPARIN-BINDING (POTENTIAL).
FT DISULFID 41 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 282 PROBABLE.
FT DISULFID 323 379 PROBABLE.
FT DISULFID 420 473 PROBABLE.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 804 1049 MISSING (IN ISOFORM N-CAM 140).
SO SEQUENCE 1088 AA; 117778 MW; 62738B5B03F3EB3 CRC64;
```

```
Query Match 10.1%; Score 116.5; DB 1; Length 1088;
Best Local Similarity 24.0%; Pred. No. 0.04;
Matches 43; Conservative 31; Mismatches 58; Indels 47; Gaps 9;
```

```
QY 18 EVATLSGHNVSVELEAQTIRYQKEKKVLTWMSGDMNIMPEYKKNRTIDITNNLSIYI 77
Db 130 EDAAVITICDVSSISIPSI---ITMRHKGKDYI-----FKKDVRFVLIANNYLQI 173
QY 78 LALRPSDEGTGYECVVLKYEKDAFRKREHLAEVTLGVKADFPPTPSISDFEI--PTSNIR- 133
Db 174 RGIKKTDEGTYYRC-----EGRIIARGEINVKDIDIVINVP-PTIQARQLRYNATANMAES 227
QY 134 -ITCSTSGGFPPEPHLSWLENGEELNAINTVSODPETELAVSSKLDPN-----MTTNH 186
Db 228 VVLSCDADGEPDPPEISWIKKGEPI-----EDGE-----EKISFNEQSEMTIHH 271
```

Search completed: June 18, 2002, 11:47:43
Job time: 226 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:32 ; Search time 26.58 Seconds

(Without alignments)
1405.828 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149
1 GLSHFGCVIHTKKEVKA.....LRVNOTFNMTTKQEHFDPN 216

Sequence: 1 GLSHFGCVIHTKKEVKA.....LRVNOTFNMTTKQEHFDPN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	97.3	288	6	077684 macaca neme
2	1100	95.7	288	6	028499 macaca mula
3	1085	94.4	288	6	09BDN6 cercocebus
4	1085	94.4	289	6	028347 cercocebus
5	764	66.5	230	6	09N213 sus scrofa
6	762.5	66.4	288	6	09TT70 sus scrofa
7	762.5	66.4	297	6	09BE99 sus scrofa
8	761	66.2	229	6	09TT71 sus scrofa
9	743	64.7	292	6	09GMZ8 felis silve
10	743	64.7	292	6	002758 felis silve
11	719	62.6	304	6	09TOX1 canis famill
12	717.5	62.4	296	6	046405 bos taurus
13	705	61.4	235	6	09TOS8 canis famill
14	705	61.4	235	6	09NOT0 canis famill
15	603.5	52.5	321	11	035187 rattus norv
16	602	52.4	290	11	062680 rattus norv

17	601.5	52.3	321	11	062624 rattus norv
18	596	51.9	321	11	055202 rattus norv
19	560	48.7	306	11	09R129 mus musculu
20	350	30.5	174	6	09GMZ9 mus musculu
21	349.5	30.4	173	6	09SL17 felis silve
22	255.5	22.2	212	11	061332 mus musculu
23	200.5	17.4	329	6	09XSK6 felis silve
24	200.5	17.4	332	6	09GMZ7 felis silve
25	200.5	17.4	332	6	09SL16 felis silve
26	188.5	16.4	280	6	09TTF1 canis famill
27	188.5	16.4	296	13	042404 gallus gall
28	182	15.8	329	6	09TTF2 canis famill
29	178	15.5	323	6	09BDM2 cercopthec
30	177	15.4	323	6	09BDM9 macaca neme
31	177	15.4	323	6	09BDM4 macaca mula
32	176	15.3	275	6	09BDN9 papio anubi
33	176	15.3	323	6	09BDN8 cercocebus
34	171	14.9	284	6	09GLJ3 bos taurus
35	162	14.1	313	11	035531 rattus norv
36	161.5	14.1	325	6	002838 sus scrofa
37	156.5	13.6	290	11	09N207 mus musculu
38	153	13.3	290	11	09EP73 mus musculu
39	153	13.3	356	11	064381 mus musculu
40	152	13.2	314	11	061238 mus musculu
41	150	13.1	309	11	091YV7 mus musculu
42	142	12.4	316	4	09BXR1 homo sapien
43	139.5	12.1	521	6	046651 oryctolagus
44	138	12.0	509	11	P97710 rattus norv
45	137	11.9	509	11	09QW15 rattus norv

ALIGNMENTS

RESULT 1

ID 077684 PRELIMINARY: PRT: 288 AA.

AC 077684; 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE B7 PROTEIN.

GN B7.

OS Macaca nemestrina (pig-tailed macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9545;

RN [1]

RP SEQUENCE FROM N.A.

RA Kraus G., Hnatyszyn J.H.;

RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF079519; AAC31555.1; --

DR InterPro: IPR003599; IG_1.

DR InterPro: IPR003600; IG_1like.

DR InterPro: IPR003006; IG_MHC.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

DR SMART: SM00410; IG_1like; 1.

```

QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 181
D 148 TDFEIPSPNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 207
QY 182 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 216
D 208 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 242

RESULT 2
Q28499 PRELIMINARY; PRT; 288 AA.
AC Q28499;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE B7 PROTEIN (CD80 PROTEIN PRECURSOR).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostlik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL: U19840; AAK6706.1; -.
DR EMBL: AF344849; AAK37609.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00410; Ig_Like; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

```

```

Query Match 95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity 96.3%; Pred. No. 2,2e-94;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 2 LSHFGSGVHTKEVKAVATLSCGHNVSEBLAOTRIYQWKEKKVLTMSGDMNIMPEY 61
D 28 LSHFGSGVHTKEVKAVATLSCGHNVSEBLAOTRIYQWKEKKVLTMSGDMNIMPEY 87
QY 62 KNRITFDITNNLSIVILALRPSDEGTGYECVYLKYEKDAFKREHLAEVTLVSKADFPPTSI 121
D 88 KNRITFDITNNLSIVILALRPSDEGTGYECVYLKYEKDAFKREHLAEVTLVSKADFPPTSI 147
QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 181
D 148 TDFEIPSPNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 207
QY 182 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 216
D 208 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 242

```

```

RESULT 3
Q9BDN6 PRELIMINARY; PRT; 288 AA.
AC Q9BDN6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE CD80 PROTEIN.
GN MNR71.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostlik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL: AF344839; AAK37535.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00410; Ig_Like; 1.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

```

```

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 5.4e-93;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 2 LSHFGSGVHTKEVKAVATLSCGHNVSEBLAOTRIYQWKEKKVLTMSGDMNIMPEY 61
D 28 LSHFGSGVHTKEVKAVATLSCGHNVSEBLAOTRIYQWKEKKVLTMSGDMNIMPEY 87
QY 62 KNRITFDITNNLSIVILALRPSDEGTGYECVYLKYEKDAFKREHLAEVTLVSKADFPPTSI 121
D 88 KNRITFDITNNLSIVILALRPSDEGTGYECVYLKYEKDAFKREHLAEVTLVSKADFPPTSI 147
QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 181
D 148 TDFEIPSPNIRRIICSTSGGPEPHLSWLENCEELNAINTVSDPELEYAVSSKLDEN 207
QY 182 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 216
D 208 MTNHSFMCILIKYGLRVNQTFFNMNTPKQEHFPDN 242

```

```

RESULT 4
Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE B7 PROTEIN (FRAGMENT).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and

```


	Query Match	61.4%	Score 705;	DB 6;	Length 235;
	Best Local Similarity	61.5%;	Pred. No.	9.7e-58;	
	Matches 128;	Conservative 33;	Mismatches 47;	Indels 0;	Gaps 0;
Oy	2 LSHFSSGVIHTKTEKKFAATLSCGGNNVSEELAQRRITWQKEKKYVLIMSGDMINIPEX 61	: :::~ : : : : : :			

RESULT	15	
035187		
ID	035187	PRELIMINARY;
AC	035187;	PRT; 321 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)
DT	01-JAN-1998	(TREMBLrel. 05, last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)
DE	B7.1.	

GN B7.1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER;
RX MEDLINE=99176848; PubMed=10078962;
RA Visse E., Siesjo P., Wiedgren B., Sjogren H.O.;
RT "Regression of intracerebral rat glioma isografts by therapeutic
RT subcutaneous immunization with interferon-gamma, interleukin-7, or
RT B7-1-transfected tumor cells";
RL Cancer Gene Ther. 6:37-44(1999).
DR EMBL; AF010465; AAB66351.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; IG_Like; 1.
SQ SEQUENCE 321 AA; 36351 MW; 071C6007FBBD1E60 CRC64;

Query Match 52.5%; Score 603.5; DB 11; Length 321;
Best Local Similarity 54.9%; Pred. No. 4.1e-48;
Matches 113; Conservative 34; Mismatches 58; Indels 1; Gaps 1;
QY 1 GLSHFCSGYI-HYTKFKVATLSCGHNVSEFLAOTRTYWKCKKVLTMMSGDNIWP 59
DB 31 GLFQISSGIVGOVSKSVREKALSCDYKFCSEOSIHRITWOKHDKMVLVSVISGVPWP 90
QY 60 EYKNRTIFDITNNLSIVILALRPSDEGTECVYLKYEKDAFKREHLAEVLSYKADPTP 119
DB 91 EYKNRTIVDIANNYSFSLGLILSDRGTYCVQRYEGESYVVKHLTVELSVRADPTP 150
QY 120 STSDFEIPTSNIRITCSGSGFPPEHLSWLENGEELNAINTVSODPETELAVSSKLD 179
DB 151 NITESGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISODPESELYTSSOLD 210
QY 180 FNMNTNHSFMCCLKYGHLELVNCTFNM 205
DB 211 FNTTYDHFIDCFIEYGDHVSQNFYW 236

Search completed: June 18, 2002, 11:47:24
Job time: 232 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:07 ; Search time 29.83 Seconds

(without alignments)
804.289 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149
Sequence: 1 GSHFCSGVHTVTKVEKVA.....LRVNGTFNNNTTQKQHFPPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802:*

- 1: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT:*
- 5: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1984.DAT:*
- 6: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1985.DAT:*
- 7: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1986.DAT:*
- 8: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1994.DAT:*
- 16: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1995.DAT:*
- 17: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1996.DAT:*
- 18: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1997.DAT:*
- 19: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	16	AA67989 Human B lymphocyte
2	1149	100.0	288	18	AAW38414 Homo sapien
3	1149	100.0	288	20	AAW67804 Human B7 protein s
4	1149	100.0	288	20	AAW73640 Human B7-2 antigen
5	1149	100.0	288	21	AAW37087 Human B lymphocyte
6	1149	100.0	288	21	AAW99966 Human B7 protein.
7	1149	100.0	288	21	AAW44289 Human B7.1 co-stim
8	1149	100.0	288	21	AAW54920 Human B7.1 protein
9	1149	100.0	288	22	AAW05121 Colorectal tumour
10	1149	100.0	288	22	AAW19959 Human B lymphocyte
11	1149	100.0	473	18	AAW41415 Human B7.1-murine

12	1146	99.7	251	20	AAW90208
13	1144	99.6	475	18	AAW38415
14	1143	99.5	488	20	AAW66004
15	1143	99.5	488	22	AAW83836
16	1143	99.5	492	19	AAW42338
17	1138	99.0	480	20	AAW90208
18	1047	91.1	208	18	AAW35858
19	1047	66.2	229	22	AAW97780
20	743	64.7	292	21	AAW32283
21	743	64.7	292	21	AAW32276
22	739	64.3	292	21	AAW32284
23	739	64.3	292	21	AAW32277
24	719	62.6	304	20	AAW41075
25	705	61.4	335	20	AAW41077
26	561	48.8	306	16	AAW82893
27	561	48.8	306	16	AAW67990
28	561	48.8	306	16	AAW19960
29	561	48.8	320	16	AAW82892
30	558	48.6	306	20	AAW67805
31	558	48.6	306	20	AAW35641
32	558	48.6	306	21	AAW37088
33	558	48.6	306	21	AAW99967
34	349.5	30.4	173	20	AAW41082
35	311	27.1	214	16	AAW82901
36	305	26.3	200	16	AAW82900
37	250.5	21.8	212	16	AAW82902
38	250.5	21.8	226	16	AAW82903
39	200.5	17.4	329	21	AAW32285
40	200.5	17.4	329	21	AAW32278
41	200.5	17.4	332	20	AAW41078
42	188.5	16.4	280	20	AAW41078
43	182	15.8	244	20	AAW90209
44	182	15.8	246	20	AAW86005
45	182	15.8	246	22	AAW83837

ALIGNMENTS

RESULT	1
ID	AAW67989 standard; Protein; 288 AA.
XX	
AC	AAW67989;
XX	
DT	21-AUG-1995 (first entry)
XX	
DE	Human B lymphocyte antigen B7-1 (hB7-1).
XX	
KW	B lymphocyte antigen; B7-1; B cell activation antigen; CD28;
KW	ligand; T cell surface antigen; transmembrane protein.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Protein
FT	Location/Qualifiers
FT	1..34
FT	/label= signal sequence
FT	/note= "hydrophobic"
FT	35..242
FT	/label= extracellular
FT	243..269
FT	/label= transmembrane
FT	270..288
FT	/label= intracellular
FT	53..55
FT	/label= N-linked glycosylation
FT	89..91
FT	/label= see above
FT	98..100
FT	/label= see above
FT	186..188
FT	/label= see above
FT	Misc-difference 207..209

hB7.1glu-solu
Soluble B7-1-19.
Human B7-1.5T4.1 p
Amino acid sequenc
CD80-Ig-alpha-tp f
hB7.1Fc soluble fu
Human B7.1 for use
Soluble porcine B7
Feline CD80 (B7-1)
Cat CD80 (B7-1)-TA
Feline CD80 (B7-1)
Cat CD80 (B7-1)-SY
Canine B7-1 protei
Canine B7-1S prote
Mouse B7-1 alterna
Murine B lymphocyt
Murine B7-1s prote
Feline B7-1 (IgV-11
Mouse B7-1 (IgV-11
Mouse B7-1 IgV-11k
Mouse B7-1 IgV-11k
Mouse B7-1 IgV-11k
Mouse B7-1 IgV-11k
Feline CD86 (B7-2)
Cat CD86 (B7-2) 11
Feline B7-2 protei
Canine B7-2s protei
hB7.1hs soluble f
Human B7-2 extrac
Amino acid sequenc

FT Misc-difference /label= see above
 FT 211..213
 FT /label= see above
 FT Misc-difference /label= see above
 FT 226..228
 FT Misc-difference /label= see above
 FT 232..234
 FT /label= see above
 FT 35..138
 FT /label= Ig V-set domain
 FT 139..236
 FT /label= Ig C-set domain
 FT
 PN WO9503408-A.
 PD 02-FEB-1995.
 PF 26-JUL-1994; 94WO-US08423.
 PR 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 XX
 PI Freeman GJ, Gray GS, Greenfield E, Nadler LM;
 DR WPI; 1995-075236/10.
 DR N-PSDB; AA081371.
 XX
 PT Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
 PT for enhancing or suppressing T-cell mediated Immune responses
 XX
 PS Disclosure; pages 111-113; 175pp; English.
 XX
 CC Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
 CC cell line Raji, clone no. 13. Its position in the genome is
 CC chromosome/segment 3. It was published by Freeman, F.J. et al.,
 CC J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be
 CC found in Genbank at accession no. M27533. The encoded protein,
 CC R67969, binds both human CTLA4 and human CD28. It is related
 CC to human hb7-2 (see Q81351) and murine hb7 (see Q81372).
 CC
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 16; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSGVYHVTKEVEVATLSGHNVSVEELAQRTIYQKEKKVLTMMSGDMNTWPE 60
 DB 27 glshfsgsvyhtvkevevatlscghnvsveelaqrtrlywqkekkmvltmmsgdmntwpe 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYERDAFKREHLAEVTLVSKADPEPTPS 120
 DB 87 yknrtifdntnlsivlilalrpsdegtyecvvlkyekdafrkhlavtlsvadpftps 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVVSQDETELYAVSSKIDF 180
 DB 147 isdfelptsnirrlficsstsggfephslswlengeelnainitlvsqdpetelyavssklidf 206
 QY 181 NMTTNSFMCLIKYGHRLRVNQTENNMTTKOEHPDN 216
 DB 207 nmttnhsfmclikyghrlrvnqtnmttkgehpdn 242

RESULT 2
 AAM38414
 ID AAM38414 standard; Protein; 288 AA.
 XX
 AC AAM38414;
 XX

DT 08-APR-1998 (first entry)
 XX
 DE B7-1.
 XX
 KW Screening; inhibitor; enhancer; binding; CD28; B7-1.
 XX
 OS Homo sapiens.
 XX
 PN EP795554-A2.
 PD 17-SEP-1997.
 PF 04-MAR-1997; 97EP-0301438.
 PR 02-OCT-1996; 96JP-0262085.
 PR 05-MAR-1996; 96JP-0047795.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 PA
 PI Hattori M, Hida T, Kurokawa T, Nakanishi A;
 PI
 DR WPI; 1997-450803/42.
 DR N-PSDB; AAT96358.
 XX
 PT New xanthene derivatives useful as immunomodulators - e.g. methyl
 PT 2-(carboxymethylsulfophenyl)-5,7-dichloro-3,8-dihydroxy-6-
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.
 XX
 PS Disclosure; Fig 4; 117pp; English.
 XX
 CC The present sequence was used in the development of a novel method
 CC for screening for compounds that inhibit or enhance binding of CD28
 CC to B7-1.
 CC
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 18; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSGVYHVTKEVEVATLSGHNVSVEELAQRTIYQKEKKVLTMMSGDMNTWPE 60
 DB 27 glshfsgsvyhtvkevevatlscghnvsveelaqrtrlywqkekkmvltmmsgdmntwpe 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYERDAFKREHLAEVTLVSKADPEPTPS 120
 DB 87 yknrtifdntnlsivlilalrpsdegtyecvvlkyekdafrkhlavtlsvadpftps 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVVSQDETELYAVSSKIDF 180
 DB 147 isdfelptsnirrlficsstsggfephslswlengeelnainitlvsqdpetelyavssklidf 206
 QY 181 NMTTNSFMCLIKYGHRLRVNQTENNMTTKOEHPDN 216
 DB 207 nmttnhsfmclikyghrlrvnqtnmttkgehpdn 242

RESULT 3
 AAM67804
 ID AAM67804 standard; Protein; 288 AA.
 XX
 AC AAM67804;
 XX
 DT 13-APR-1999 (first entry)
 DE Human B7 protein sequence.
 DE
 XX
 KW Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
 KW T-cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
 XX
 OS Homo sapiens.
 XX

```

FH Key Location/Qualifiers
FT Peptide 1..34
FT Protein /note= "signal peptide"
FT Protein 35..288
FT Domain /note= "mature B7 protein"
FT Domain 35..242
FT Domain /note= "extracellular domain"
FT Domain 243..269
FT Domain /note= "transmembrane domain"
FT Domain 270..288
FT Domain /note= "intracellular domain"
FT Modified-site 53..55
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 89..91
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 98..100
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 186..188
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 207..209
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 211..213
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 226..228
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 236..234
FT Modified-site /note= "Asn is N-glycosylated"
FT Domain 35..139
FT Domain /note= "Ig V-set domain"
FT Domain 140..236
FT Domain /note= "Ig C-set domain"
FN US5858776-A.
PN 12-JAN-1999.
PD 03-NOV-1993; 93US-0147772.
PE 03-NOV-1993; 93US-0147772.
PR 03-NOV-1993; 93US-0147772.
XX (DAND ) DANA FARBER CANCER INST INC.
PA (HARD ) HARVARD COLLEGE.
PA (REPK ) REPLIGEN CORP.
PI Baekar S, Freeman GJ, Glimcher LH, Nadler LM, Ostrand-Rosenberg S;
XX WPI: 1999-119893/10.
DR N-PSDB: AAX00757.
XX
PT New modified tumour cells - transfected in order to express a T cell
PT costimulatory molecule which allows the induction of an anti-tumour
PT response by T cells
XX
PS Disclosure: Column 31-34; 24pp; English.
XX
CC This sequence represents the amino acid sequence of a human B7 protein.
CC The coding sequence can be used to transfect mammalian tumour (sarcoma)
CC cell so that the B7 protein is expressed by the tumour cell and has the
CC ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.
CC The modified tumour cells can be used for inducing an anti-tumour
CC T-lymphocyte response in a subject and are effective against both
CC modified and unmodified tumour cells. The modified tumour cells can
CC also be administered to prevent or inhibit metastatic spread of a tumour
CC or to prevent or inhibit recurrence of a tumour following therapeutic
CC treatment.
CC
SQ Sequence 288 AA:

```

```

Query Match 100.0%; Score 1149; DB 20; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GLSHFCGVIVHTKEVKEVATLSCGHNVSVBELAQTRITWQKEKKVLTMMSGDMNIPE 60
DB 27 glshfcsgviviltkvkevatlscghnsvsvelaqtiriywqkekkmvltmmsgdmniwpe 86
OY 61 YKNRTIEDITNNLSIVIALRPSDEGTIECVYLKREKAFKREHLAEVTLVKADFPPTS 120
DB 87 yknrtiefditnnlsivialrpsdegtyecvylkyekdafkrehlaevtlsvkadfppts 146
OY 121 ISDFEIPSNIRRICSGSGPEPHLSMLENGEELNINFTVSDPEPELYAVSSKIDF 180
DB 147 isdfelpsnirrlscsgsgfpephlsmlengeelnaftvsgdpeelyavsskidf 206
OY 181 NMTNHSFMCILIKYGHLELVNQTFFNMNTTKOEHPDN 216
DB 207 nmtnhsfmcilkyghlrvnqtfnmnttkgehfdn 242

RESULT 4
AAW73640
ID AAW73640 standard; Protein: 288 AA.
XX
AC AAW73640;
XX
DT 23-MAR-1999 (first entry)
XX
DE Human B7-2 antigen.
XX
KW B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KW CTLA4 ligand; therapy; T-cell response; human.
XX
OS Homo sapiens.
XX
PN US5861310-A.
XX
PD 19-JAN-1999.
XX
PE 30-MAY-1995; 95US-0456104.
XX
PR 30-MAY-1995; 95US-0456104.
PR 03-NOV-1993; 93US-0147773.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Freeman GJ, Gray GS, Nadler LM;
XX
DR WPI: 1999-130394/11.
DR N-PSDB: AAV55786.
XX
PT Tumour cell transfected to express B7-2 molecule - useful for tumour
PT therapy by stimulating T-cell response
XX
PS Disclosure: Column 37-40; 27pp; English.
XX
CC This sequence is the human B7-2 antigen, which can be used in the
CC method of the invention. The method is for transfecting an isolated
CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC tumour cell is capable of costimulating a T cell and is capable of
CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC by stimulating a T-cell response against tumour cells in vivo.
XX
SQ Sequence 288 AA:

```

```

Query Match 100.0%; Score 1149; DB 20; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GLSHFCGVIVHTKEVKEVATLSCGHNVSVBELAQTRITWQKEKKVLTMMSGDMNIPE 60
DB 27 glshfcsgviviltkvkevatlscghnsvsvelaqtiriywqkekkmvltmmsgdmniwpe 86
OY 61 YKNRTIEDITNNLSIVIALRPSDEGTIECVYLKREKAFKREHLAEVTLVKADFPPTS 120

```

Db 87 yknrtfditnmslvllaalrpsdegtyecvvlkyekdafkrehlavelsvradptps 146
 QY 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLNGBELNAINTVSODPETELAVSSKIDF 180
 Db 147 Isdfelptsnirrlrictsgsgfpephlswlengelaaintvsgdpetelavssklidf 206
 QY 181 NMTTNHSEFMCLIKYGHRLVNOTFNWNTTKOEHFDPN 216
 Db 207 nmttnhsfmclikyghrlvnotfnwnttkqehfpdn 242

RESULT 5
 ID AAB37087 standard; Protein; 288 AA.
 XX AAB37087;
 AC
 XX 28-MAR-2001 (first entry)
 DT
 XX Human B lymphocyte antigen B7-1.
 DE
 XX Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
 KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
 KW T cell-mediated immune response; transplantation; vaccination.
 XX
 OS Homo sapiens.
 XX
 PN US6130316-A.
 PD 10-OCT-2000.
 XX
 PF 26-JUL-1994; 94US-0280757.
 XX
 PR 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;
 XX WPI: 2000-655681/63.
 DR N-PSDB; AAC84051.
 XX
 PT Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
 PT enhancing or suppressing T cell-mediated immune responses, especially
 PT during tissue, skin or organ transplantation, or in graft-versus-host
 PT disease -
 PS Disclosure: Column 87-90; 83pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule encoding a
 CC fusion protein comprising a first nucleotide sequence encoding a first
 CC peptide, and a second nucleotide sequence encoding a second peptide.
 CC The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
 CC to a portion of a nucleotide sequence which encodes a human or murine
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid
 CC sequence that is identical or at least 50% identical with the
 CC extracellular domain of a human B7-2 peptide (AAB37087). The second
 CC peptide is especially an immunoglobulin constant region. This sequence
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example
 CC of a first peptide sequence of the invention. The nucleic acid molecules
 CC are useful in various expression vectors to direct synthesis of the
 CC corresponding proteins or peptides in a variety of hosts, particularly
 CC eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
 CC acids are also useful for enhancing the immunogenicity of a mammalian
 CC cell, e.g. tumour cell (sarcoma) or an antigen presenting cell

CC (macrophage). The fusion proteins or peptides are useful for enhancing or
 CC suppressing T cell-mediated immune responses, e.g. in situations of
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.
 CC The proteins are also useful for enhancing the efficacy of vaccination
 CC against a variety of pathogens, and may also be used to upregulate an
 CC immune response against a particular pathogen during an infection or
 CC against a tumour in a tumour-bearing host.
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2,6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGGVHWTKEVKEVATLSCGHNVSEELAQTRITYWKEKKMVLTMNSGDMNIMPE 60
 Db 27 glshfsgvhlwtkevekatlscghnvseelaqtritywqekkmvltmnsghdmniwpe 86
 QY 61 YKNRTFDITNNSIVLALRPSDEGTVECVLKYEKDAFKREHLAEVTLISKADFPPTPS 120
 Db 87 yknrtfditnmslvllaalrpsdegtyecvvlkyekdafkrehlavelsvradptps 146
 QY 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLNGBELNAINTVSODPETELAVSSKIDF 180
 Db 147 Isdfelptsnirrlrictsgsgfpephlswlengelaaintvsgdpetelavssklidf 206
 QY 181 NMTTNHSEFMCLIKYGHRLVNOTFNWNTTKOEHFDPN 216
 Db 207 nmttnhsfmclikyghrlvnotfnwnttkqehfpdn 242

RESULT 6
 ID AAY99966 standard; Protein; 288 AA.
 XX AAY99966;
 AC
 XX 10-JAN-2001 (first entry)
 DT
 XX Human B7 protein.
 DE
 XX B7; human; B cell activation antigen; B lymphocytes;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW herpes simplex; influenza; common cold; HIV.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..34
 FT Domain 35..242
 FT /label= Extracellular_domain
 FT Domain 35..138
 FT /label= "Ig V-set domain"
 FT Modified-site 53..55
 FT /note= "N-linked glycosylation site"
 FT Modified-site 89..91
 FT /note= "N-linked glycosylation site"
 FT Modified-site 98..100
 FT /note= "N-linked glycosylation site"
 FT Domain 139..236
 FT /label= "Ig C-set domain"
 FT Modified-site 186..188
 FT /note= "N-linked glycosylation site"
 FT Modified-site 207..209
 FT /note= "N-linked glycosylation site"
 FT Modified-site 211..213
 FT /note= "N-linked glycosylation site"
 FT Modified-site 226..228
 FT /note= "N-linked glycosylation site"
 FT Modified-site 232..234
 FT /note= "N-linked glycosylation site"


```

FT      Domain                243..269
FT      /label= Transmembrane_domain
FT      Domain                270..288
FT      /label= Intracellular_domain
XX      US6071716-A.
XX      PD
XX      06-JUN-2000.
XX      PE
XX      15-NOV-1993; 93US-0153262.
XX      PR
XX      28-AUG-1991; 91US-0751306.
XX      PR
XX      01-OCT-1990; 90US-0591300.
XX      XX
XX      (DAND ) DANA FARBER CANCER INST INC.
XX      PI
XX      Nadler LM, Freeman GJ, Freedman AS;
XX      WPI; 2000-422081/36.
XX      DR
XX      N-PSDB; AAA61328.
XX      PS
XX      Claim 1; Fig 4; 36pp; English.
XX      PT
XX      New polynucleotides encoding a B7 activation antigen, useful for
XX      regulating T cell mediated immune responses or viral diseases -
XX      XX
XX      The present sequence is the unique human B cell activation antigen B7
XX      protein. The cDNA encoding this sequence was isolated from a Burkitt
XX      lymphoma cell line cDNA library. Selection of cDNA clones was based
XX      on expression of B7, as detected by the anti-B7 monoclonal antibody.
XX      The human B7 cDNA was used in hybridisation analysis to isolate the
XX      murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
XX      used to generate transgenic, knock-out animals which, in turn, are
XX      useful in the development and screening of therapeutically useful
XX      reagents. The expressed B7 protein is useful for enhancing or
XX      blocking activated T cell mediated immune responses and immune
XX      function. Modification of B7 expression is useful in the treatment of
XX      autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
XX      herpes simplex, influenza, the common cold and HIV. It is also useful
XX      in tissue and organ transplantation.
XX      CC
XX      Sequence 288 AA:
SQ
Query Match 100.0%; Score 1149; DB 21; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVEKVALSCGHNVSEELAQTRITYQKEKKVLTMMSGDMNIWPE 60
DB 27 glshfcsgvihvtkevkevalscghnvsveelaqtritywqekkmvltmmsgdmniwpe 86
QY 61 YKNRTIFDTNNLSVIALRPSDGTGYECVYLKYEKDAFKREHLAEVTLISKADFPPTS 120
DB 87 yknrtifdtnnlsvialrpsdgtgyecvylkyekdafkrehlaevtlisvskadfppts 146
QY 121 ISDFEIPISNRIIRICSTSGGPEPHLSWLENGEELNAINITVSQDEPETELAVSSKIDF 180
DB 147 isdfepisnriiricstsggpephlswlengeelnaaintvsqdepetylavsskldf 206
QY 181 NMTNHSFMCILKYGHLRVNQTFFNMNTTKQEHFPDN 216
DB 207 nmtnhsfmcilkyghlrvnqtfnmnttkqehfpdn 242

```

```

RESULT 7
AAV44289
ID AAV44289 standard; Protein; 288 AA.
XX
AC AAV44289;
XX
DT 29-FEB-2000 (first entry)
XX

```

```

DE      Human B7.1 co-stimulatory molecule.
XX      XX
XX      Human B7.1 co-stimulatory molecule; antigen presenting cell;
XX      immune response; cell surface receptor; Major histocompatibility complex;
XX      MHC classII; proton motor force; mitochondrial membrane potential;
XX      mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
XX      neurodegenerative disorder.
XX      OS
XX      Homo sapiens.
XX      PN
XX      WO953953-A2.
XX      PD
XX      28-OCT-1999.
XX      PE
XX      30-MAR-1999; 99WO-US06874.
XX      PR
XX      17-APR-1998; 98US-0082250.
XX      PR
XX      29-JUL-1998; 98US-0094519.
XX      PR
XX      24-SEP-1998; 98US-0101580.
XX      XX
XX      (UYVE-) UNIV VERMONT.
XX      PI
XX      Newell MK;
XX      WPI; 2000-096773/08.
XX      DR
XX      N-PSDB; AA229320.
XX      PT
XX      Use of cell surface and membrane characteristics for developing
XX      products for treating cancers, autoimmune diseases or neurodegenerative
XX      diseases -
XX      XX
XX      Disclosure; Page 115; 133pp; English.
XX      CC
XX      The present sequence is human B7.1 co-stimulatory molecule. This is
XX      a glycoprotein on the surface of antigen presenting cells. This is
XX      involved in stimulation of an immune response by its ability to interact
XX      with various immune cell surface receptors. The regulation of cell
XX      surface expression of MHC classII and co-stimulatory molecule B7 can be
XX      manipulated by regulating the intracellular dissipation of proton motor
XX      force which can be assessed in terms of mitochondrial membrane potential.
XX      These methods can be used for regulating cell growth and division to
XX      control disease processes by manipulating mitochondrial metabolism and
XX      the expression of cell surface immune proteins. They can be used for
XX      treating diseases associated with excessive cellular division, aberrant
XX      differentiation, and premature cellular death, e.g. cancers, autoimmune
XX      diseases, neurodegenerative disorders etc.
XX      CC
XX      Sequence 288 AA:
SQ
Query Match 100.0%; Score 1149; DB 21; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVEKVALSCGHNVSEELAQTRITYQKEKKVLTMMSGDMNIWPE 60
DB 27 glshfcsgvihvtkevkevalscghnvsveelaqtritywqekkmvltmmsgdmniwpe 86
QY 61 YKNRTIFDTNNLSVIALRPSDGTGYECVYLKYEKDAFKREHLAEVTLISKADFPPTS 120
DB 87 yknrtifdtnnlsvialrpsdgtgyecvylkyekdafkrehlaevtlisvskadfppts 146
QY 121 ISDFEIPISNRIIRICSTSGGPEPHLSWLENGEELNAINITVSQDEPETELAVSSKIDF 180
DB 147 isdfepisnriiricstsggpephlswlengeelnaaintvsqdepetylavsskldf 206
QY 181 NMTNHSFMCILKYGHLRVNQTFFNMNTTKQEHFPDN 216
DB 207 nmtnhsfmcilkyghlrvnqtfnmnttkqehfpdn 242

```

```

RESULT 8
AAV54920

```

ID AAY54920 standard; Protein; 288 AA.
 XX AAY54920;
 AC
 XX 14-FEB-2000 (first entry)
 DT
 XX Human B7.1 protein sequence.
 DE
 XX Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
 KM IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
 XX
 OS Homo sapiens.
 XX
 PN US9594104-A.
 PD 30-NOV-1999.
 XX
 PF 08-NOV-1996; 96US-0751767.
 XX
 PR 08-NOV-1996; 96US-0751767.
 XX
 PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 PI Anderson RJ, Prentice HG, MacDonald ID;
 DR N-PSDB; AAZ40022.
 XX
 PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
 PT for treating leukemia and other cancers -
 XX
 PS Example; Fig 10; 73pp; English.
 XX
 CC This sequence represents the human B7.1 protein sequence.
 CC The invention relates to an isolated nucleic acid construct (1)
 CC comprising a region encoding an interleukin-12 (IL-12) fusion protein
 CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker
 CC peptide (joining the subunits)) and a region encoding a B7 protein. (1)
 CC may be used to produce IL-12 fusion proteins according to standard
 CC recombinant DNA methodologies. The fusion proteins may be produced either
 CC in vitro in a fermentation culture or in vivo as part of a gene therapy
 CC protocol (in this case (1) is used to transform a patient's cells, which
 CC then secrete the functional polypeptide to supplement the patients own
 CC production of IL-12 or to rectify mutations which lead to the expression
 CC of inactive polypeptides). The fusion proteins produced in this way may
 CC be used to treat any disease which responds to IL-12 such as tumours
 CC (both solid and dispersed of the kidney, breast, colon, ovarian and
 CC cervical tumours and melanomas) and in particular, tumours of the blood
 CC such as leukaemia. Alternatively, the polypeptides may be used as
 CC antigens in the production of antibodies to IL-12 and to assay for
 CC agonists and antagonists of its activity. The antibodies and antagonists
 CC may be used to inhibit the activity of IL-12. (1) may also be used
 CC diagnostically as a probe which hybridizes to sequences encoding IL-12
 CC and the antibodies may be used to detect the presence of IL-12
 CC polypeptides in samples. They may be used diagnostically to quantitate
 CC the expression of the polypeptide by patients and hence which subjects
 CC may be in need of restorative therapy.
 CC
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHRCGVVHTWTKKEVATLSCGHNVSVEELAQRIRYKREKKVLLMMSGDMNIMPE 60
 DB 27 gshrcsgvvhvtrkvekatlscghnvsveelagrtrlywqekkmvllmmsgdmniwpe 86
 QY 61 YKNRIITFDITNNLSYIIALRPSDEGTVECVVLKYEKDAFKREHLAEVTLVYKADFPPTS 120
 DB 87 yknrtifdtlnlslvialrpsdegtyecvvlkyekdafkrehaevlsvkadtptps 146

QY 121 ISDFEIPTSNIRRIICSTSGCFPEPHLSWLENGEELINAIINTVSODPETELVAVSSKIDF 180
 DB 147 isdfepstsnirrllostsgtfpephlswlengeeelnainatltvsqdpetelyavsskldf 206
 QY 181 NMTTNHSEFMCLIRYGHILRVNQTFFNNNTTQKQHEPPDN 216
 DB 207 nmttnhsfmclirkyghilrvnqtfnnnttqkqhefpdn 242

RESULT 9

AAU05121 standard; Protein; 288 AA.
 ID AAU05121
 AC AAU05121;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Colorectal tumour antigen CD80.
 XX
 KM Colorectal cancer; immunostimulant; cytostatic; immune response;
 KM adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;
 KM SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
 KM tumour antigen CD80.
 XX
 OS Homo sapiens.
 XX
 PN WO200154716-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-0502731.
 XX
 PR 27-JAN-2000; 2000US-0178498.
 PR 28-FEB-2000; 2000US-0185335.
 XX
 PA (KIMM-) KIMMEL CANCER CENT SYDNEY.
 PA (IMM-) IMMUNE RESPONSE CORP.
 XX
 PI Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
 DR N-PSDB; AAS11426.
 XX
 PT New composition comprising an allogeneic tumour cell, useful for
 PT stimulating an immune response in a patient having an adenocarcinoma,
 PT especially useful for treating colorectal, breast, lung or prostate
 PT cancer -
 XX
 PS Example 2; Page 130-131; 131pp; English.
 XX
 CC The invention relates to a composition for stimulating an immune response
 CC in a patient having an adenocarcinoma or colorectal cancer. The
 CC composition comprises an allogeneic tumour cell selected from SW620 cell,
 CC COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
 CC cell stimulates an immune response to an autologous tumour cell in the
 CC patient. The composition is useful for stimulating an immune response in
 CC a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
 CC adenocarcinoma. The use of allogeneic tumour cells provides a generic
 CC source of antigen that can be administered to a variety of patients, in
 CC contrast to using autologous tumour cells, which must be isolated from
 CC each individual patient. The allogeneic cells are suitable as a cancer
 CC vaccine and can stimulate an immune response against autologous tumour
 CC cells of a cancer patient. The present sequence represents the amino acid
 CC sequence of colorectal tumour antigen CD80 used in the method of the
 CC invention.
 CC
 XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUSHFCSGYIHWTKVEKVEATLSCGHNSVEBELAQTRIMQKREKKNVLTMMSGDNIMPE 60
 |||||||
 Db 27 gshfcsgyihwtkeveatlscghnsvveelaqtriywqekkmvlmmgdmniwpe 86
 |||||||
 QY 61 YKNRTIFDTNNLSYIILALRPSDEGTVCYVLYKREKDAFKREHIAEVLTSKADFPPTS 120
 |||||||
 Db 87 YNRTIFDTNNLSYIILALRPSDEGTVCYVLYKREKDAFKREHIAEVLTSKADFPPTS 146
 |||||||
 QY 121 ISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAINTVSODPETELAYAVSSKIDF 180
 |||||||
 Db 147 ISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAINTVSODPETELAYAVSSKIDF 206
 |||||||
 QY 181 NMTNHSFMCILIKYGHILRVNQTFFNNNTKQEHFPDN 216
 |||||||
 Db 207 mlttnhsfmcilikyghilrvnqtfnnntkqehfpdn 242
 |||||||

RESULT 10
 AAB19959
 ID AAB19959 standard; Protein; 288 AA.
 XX
 AC AAB19959;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Human B lymphocyte antigen B7.
 XX
 KW Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
 KW CD8; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
 KW metastasis; antitumour; therapy.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FH 1..34
 FT Peptide /label- signal_peptide
 FT 35..288
 FT Protein /label- Mature_protein
 FT 35..242
 FT Domain /note= "extracellular domain"
 FT 243..269
 FT Domain /note= "transmembrane domain"
 FT 270..288
 FT Domain /note= "intracellular domain"
 FT 35..138
 FT Domain /note= "immunoglobulin V-set domain"
 FT 139..236
 FT Domain /note= "immunoglobulin C-set domain"
 FT 53..55
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 89..91
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 98..100
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 186..188
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 207..209
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 211..213
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 226..228
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 232..234
 FT Modified-site /note= "Asn is N-glycosylated"
 FT
 XX US6149905-A.
 PN
 XX 21-NOV-2000.
 PD
 XX 23-SEP-1998; 98US-0159135.
 PF
 XX 03-NOV-1993; 93US-0147772.
 PR
 XX

PA (GENY) GENETICS INST INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
 PI Nadler LM;
 DR WPI: 2001-079388/09.
 DR N-PSDB: AAA89224.
 XX
 PT Modifying tumor cell for treating tumors, reducing metastatic spread,
 PT inhibiting recurrence of tumor and increasing immunogenicity. Involves
 PT transfecting tumor cells with a nucleic acid encoding B7 molecule
 XX
 PS Claim 4; Column 31-34; 24pp; English.

CC The present sequence is that of human lymphocyte antigen B7, a T
 CC cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
 CC cells modified to express a T cell costimulatory molecule,
 CC especially B7, are disclosed. The tumour cells are modified by
 CC transfection with a nucleic acid encoding the T cell costimulatory
 CC molecule, by using an agent which induces or increases expression
 CC of the T cell costimulatory molecule on the tumour cell surface, or
 CC by coupling the T cell costimulatory molecule to the tumour cell
 CC surface. Tumour cells further modified to express major
 CC histocompatibility complex (MHC) class I and/or class II molecules,
 CC or in which expression of an MHC associated protein, the invariant
 CC chain, is inhibited are also disclosed. The modified tumour cells
 CC are used to treat a patient with a tumour, preventing or inhibiting
 CC metastatic spread or tumour recurrence. The tumour may be a
 CC melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
 CC specifically inducing a CD4+ T cell response against a tumour, and a
 CC method for treating a tumour by modification of tumour cells in vivo
 CC are also disclosed. The treatment methods increase the immunogenicity
 CC of the tumour cell in vivo. The antitumour T cell-mediated immune
 CC response is effective both against the modified tumour cells and the
 CC unmodified tumour cells from which the modified cells were derived.
 CC Thus, the effector phase of the antitumour response induced by the
 CC modified tumour cells is not dependent upon expression of a
 CC costimulatory molecule on the tumour cells.

Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUSHFCSGYIHWTKVEKVEATLSCGHNSVEBELAQTRIMQKREKKNVLTMMSGDNIMPE 60
 |||||||
 Db 27 gshfcsgyihwtkeveatlscghnsvveelaqtriywqekkmvlmmgdmniwpe 86
 |||||||
 QY 61 YKNRTIFDTNNLSYIILALRPSDEGTVCYVLYKREKDAFKREHIAEVLTSKADFPPTS 120
 |||||||
 Db 87 YNRTIFDTNNLSYIILALRPSDEGTVCYVLYKREKDAFKREHIAEVLTSKADFPPTS 146
 |||||||
 QY 121 ISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAINTVSODPETELAYAVSSKIDF 180
 |||||||
 Db 147 ISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAINTVSODPETELAYAVSSKIDF 206
 |||||||
 QY 181 NMTNHSFMCILIKYGHILRVNQTFFNNNTKQEHFPDN 216
 |||||||
 Db 207 mlttnhsfmcilikyghilrvnqtfnnntkqehfpdn 242
 |||||||

RESULT 11
 AAM41415
 ID AAM41415 standard; Protein; 473 AA.
 XX
 AC AAM41415;
 XX
 DT 02-JUN-1998 (first entry)
 PR
 XX

DE Human B7.1-murine A5b7 F(ab')₂ fusion protein.
XX
XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
XX WO9742329-A1.
XX
XX 13-NOV-1997.
XX
XX 29-APR-1997; 97WO-GB01165.
XX
XX 14-FEB-1997; 97GB-0003103.
XX 04-MAY-1996; 96GB-0009405.
XX
XX (ZENE) ZENECA LTD.
XX
XX Copley CG, Edge MD, Emery SC;
XX
XX WPI: 1997-558987/51.
XX N-PSDB: AAV17340.
XX
XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT diagnosis and therapy of cancer
XX
XX Reference Example 3; Page 190-193; 208pp; English.
XX
XX This sequence is the human B7.1-murine A5b7 F(ab')₂ fusion protein
CC (Ab'), and is an example of the antibody of the invention. The antibody
CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably
CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA
CC encoding the antibody, are used to make the antibody or conjugate. The
CC conjugate is used in a medicament suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The conjugate can be used for in vivo or in vitro
CC diagnosis of cancer.
XX
XX Sequence 473 AA:
SQ
Query Match 100.0%; Score 1149; DB 18; Length 473;
Best Local Similarity 100.0%; Pred. No. 5.3e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHFSGVIVHTREKVEKVAATLSCGHNVSEELAQTRIVQKREKMYLTMMSGDMNIMPE 60
DB 27 glshfsgvvhvckevatlscghnsvaelaqrlywqkekmyltmmsgdmniwpe 86
QY 61 YKRRITFDITNNSTIYLALRPSDEGYECVYLKYEKDAFRHLAEVTLVSKADFPPTS 120
DB 87 ykrritfditnnstiyllalrpsdegylcvlkyekdkrhlaelvllsvkadfppts 146
QY 121 ISDFEIPTSNIRRICSTSGGPEPHLSWLENGEELNAINTVSDPETELAVASSKIDF 180
DB 147 isdfelptsnirricstsggfpelhlswlengelnaaintvsgdpetelyavasskidf 206
QY 181 NMTNHSFMCILIKYGHILRVNQTENMNTTKQEHFPDN 216
DB 207 nmctnhsfmcilikyghilrvnqtfenmttkqehfpdn 242
RESULT 12
AAW90208
ID AAW90208 standard; Protein: 251 AA.
XX
XX AAW90208:
AC
XX 10-MAY-1999 (first entry)
DT
XX hb7.1glu-glu soluble fusion protein.
DE

KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy: human; hb7.1glu-glu.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
XX Key Location/Qualifiers
FH 1..34
FT /note= "potential eukaryotic secretory signal
FT Peptide"
FT
FT Domain 35..242
FT /note= "human B7.1 (mature protein) extracellular
FT domain"
FT 243..251
FT /note= "Glu-Glu detection/purification tag"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection
XX
XX Example 3.1.2; Fig 4; 182pp; English.
XX
XX This 29 kDa soluble fusion protein, termed hb7.1glu-glu, is composed
CC of human co-stimulatory molecule B7.1 extracellular domain fused
CC C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It
CC was produced from total RNA of Epstein-Barr virus-transformed
CC human spleen cells by RT-PCR using primers MR67 and MR145 (see
CC AAX01601). The fusion protein has been produced in Sf9 Spodoptera
CC frugiperda insect cells using a baculovirus expression system.
CC The invention relates to molecules such as diabodies, trivalent and
CC tetravalent antibodies and small antigen binding peptides which can
CC cross-link, or cross-react with, B7.1 and B7.2 expressed on
CC professional antigen presenting cells leading to the inhibition of
CC antigen-specific T cell activation. Methods to produce such
CC molecules are provided. The molecules are used to treat or prevent
CC diseases of the immune system, in particular graft rejection, graft
CC versus host disease, allergy and autoimmune diseases (claimed).
XX
XX Sequence 251 AA:
SQ
Query Match 99.7%; Score 1146; DB 20; Length 251;
Best Local Similarity 99.5%; Pred. No. 4.2e-103;
Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHFSGVIVHTREKVEKVAATLSCGHNVSEELAQTRIVQKREKMYLTMMSGDMNIMPE 60
DB 27 glshfsgvvhvckevatlscghnsvaelaqrlywqkekmyltmmsgdmniwpe 86
QY 61 YKRRITFDITNNSTIYLALRPSDEGYECVYLKYEKDAFRHLAEVTLVSKADFPPTS 120
DB 87 ykrritfditnnstiyllalrpsdegylcvlkyekdkrhlaelvllsvkadfppts 146
QY 121 ISDFEIPTSNIRRICSTSGGPEPHLSWLENGEELNAINTVSDPETELAVASSKIDF 180
DB 147 isdfelptsnirricstsggfpelhlswlengelnaaintvsgdpetelyavasskidf 206
QY 181 NMTNHSFMCILIKYGHILRVNQTENMNTTKQEHFPDN 216

DB 207 nmtnhsfmclykghlyvqfntwtkqghpdpn 242

RESULT 13

AAW86415

ID AAW86415 standard; Protein; 475 AA.

AC AAW86415;

XX 08-APR-1998 (first entry)

DE Soluble B7-1-Ig.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1;

XX Soluble B7-1-Ig; immunoglobulin.

OS Homo sapiens.

XX EP795554-A2.

XX 17-SEP-1997.

XX 04-MAR-1997; 97EP-0301438.

XX 02-OCT-1996; 96JP-0262085.

XX 05-MAR-1996; 96JP-0047795.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hattori M, Hida T, Kurokawa T, Nakanishi A;

XX WPI; 1997-450803/42.

XX N-PSDB; AAT96359.

XX New xanthene derivatives useful as immunomodulators - e.g. methyl

XX 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-

XX methyl-9-oxo-9H-xanthene-1-carboxylate.

XX Disclosure; Fig 6 and 7; 117pp; English.

XX The present sequence was used in the development of a novel method

XX for screening for compounds that inhibit or enhance binding of CD28

XX to B7-1.

XX Sequence 475 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

AAW86004;

XX 15-MAR-1999 (first entry)

XX Human B7-1.5T4.1 protein fusion, specific for human 5T4.

XX Tumour interacting protein; cancer; gene therapy; vector;

XX 5T4 antigen; monoclonal antibody; single chain antibody;

XX mouse; human; B7-1; co-stimulatory molecule.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX Chimeric - synthetic.

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB01627.

XX 04-JUL-1997; 97GB-0014230.

XX 04-JUN-1997; 97GB-001579.

XX 20-JUN-1997; 97GB-0013150.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;

XX Myers KA;

XX WPI; 1999-059910/05.

XX N-PSDB; AAW80292.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

AAW86004; 15-MAR-1999 (first entry)

XX Human B7-1.5T4.1 protein fusion, specific for human 5T4.

XX Tumour interacting protein; cancer; gene therapy; vector;

XX 5T4 antigen; monoclonal antibody; single chain antibody;

XX mouse; human; B7-1; co-stimulatory molecule.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX Chimeric - synthetic.

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB01627.

XX 04-JUL-1997; 97GB-0014230.

XX 04-JUN-1997; 97GB-001579.

XX 20-JUN-1997; 97GB-0013150.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;

XX Myers KA;

XX WPI; 1999-059910/05.

XX N-PSDB; AAW80292.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELAVSSKIDF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELAVSSKIDF 206
 QY 181 NMNTNHSFMCILIKYGHURVNOTFMNNTTKOEHFPD 215
 DB 207 nmctnhsfmcilkyghlrvnqtlmwtckgehpD 241

RESULT 15
 AAB83836
 AAB83836 standard; Protein; 488 AA.
 AAB83836;
 23-JUL-2001 (first entry)

DE Amino acid sequence of a B7-1.574.1 fusion protein.
 XX Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder.
 XX Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 OS
 XX WO200136486-A2.
 PN 25-MAY-2001.
 XX
 PD 13-NOV-2000; 2000WO-GB04317.
 XX
 PF 18-NOV-1999; 99MO-GB03859.
 PR 15-FEB-2000; 2000GB-0003527.
 PR 02-MAR-2000; 2000GB-0005071.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 PI Myers KA;
 XX
 DR N-PDB; AAF89730.
 XX
 DR WPI; 2001-343805/36.
 XX
 XX
 PT Use of single chain antibody capable of recognizing a disease
 PT associated molecule for manufacturing a medicament for preventing
 PT and/or treating a disease condition associated with disease associated
 PT molecule -
 XX
 XX
 PS Claim 3; Fig 2; 118pp; English.
 XX
 CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a
 CC disease condition. The ScFv antibody is useful in the manufacture of
 CC a medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for
 CC treating inflammatory diseases including arthritis, hypersensitivity,
 CC autoimmune diseases, cancers, central nervous system disorders
 CC including Parkinson's disease, periodontal diseases, cardiopulmonary
 CC diseases, cardiovascular diseases, gastrointestinal disorders,
 CC infections, diabetes, Helicobacter-related diseases, and other immune
 CC disorders. The present sequence represents a B7-1.574.1 fusion protein.
 CC This comprises the N-terminus of the 574 ScFv is fused after amino acid
 CC 215 of human B7-1.
 CC
 XX
 SQ Sequence 488 AA;

Query Match 99.5%; Score 1143; DB 22; Length 488;
 Best Local Similarity 100.0%; Pred. No. 2.1e-102;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHFSGVTHWTKKEKAVATLSCGHNVSVEELAQRTIYQKEKKMYLTMMSGDMNIMPE 60
 DB 27 gshfsgvthwtkkevavatlscghnvsveelaqrtilyqkkekmylmmsgdmn1wpe 86
 QY 61 YKNRTTFDITNNLSIVILALRPSDEGTVECVLTKYKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 yknrttfdtitnnlsivilalrpsdegtyecvltkkyekdafkrehlaevtlsvkadfppts 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELAVSSKIDF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELAVSSKIDF 206
 QY 181 NMNTNHSFMCILIKYGHURVNOTFMNNTTKOEHFPD 215
 DB 207 nmctnhsfmcilkyghlrvnqtlmwtckgehpD 241

Search completed: June 18, 2002, 11:44:32
 Job time: 85 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:07 ; Search time 107.98 Seconds

(Without alignments)
704.092 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149
Sequence: 1 GLSHRCSEVHTKEKEVA.....LRVNOTFMWNTKQHPFDN 216

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US102_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US103_COMB.pep:*
27: /cgn2_6/ptodata/2/paa/US104_COMB.pep:*
28: /cgn2_6/ptodata/2/paa/US105_COMB.pep:*
29: /cgn2_6/ptodata/2/paa/US106_COMB.pep:*
30: /cgn2_6/ptodata/2/paa/US107_COMB.pep:*
31: /cgn2_6/ptodata/2/paa/US108_COMB.pep:*
32: /cgn2_6/ptodata/2/paa/US109_COMB.pep:*
33: /cgn2_6/ptodata/2/paa/US110_COMB.pep:*
34: /cgn2_6/ptodata/2/paa/US111_COMB.pep:*
35: /cgn2_6/ptodata/2/paa/US112_COMB.pep:*
36: /cgn2_6/ptodata/2/paa/US113_COMB.pep:*
37: /cgn2_6/ptodata/2/paa/US114_COMB.pep:*
38: /cgn2_6/ptodata/2/paa/US115_COMB.pep:*
39: /cgn2_6/ptodata/2/paa/US116_COMB.pep:*
40: /cgn2_6/ptodata/2/paa/US117_COMB.pep:*
41: /cgn2_6/ptodata/2/paa/US118_COMB.pep:*
42: /cgn2_6/ptodata/2/paa/US119_COMB.pep:*
43: /cgn2_6/ptodata/2/paa/US120_COMB.pep:*
44: /cgn2_6/ptodata/2/paa/US121_COMB.pep:*
45: /cgn2_6/ptodata/2/paa/US122_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	216	8	US-08-459-766B-8
2	1149	100.0	216	19	US-09-569-164A-8
3	1149	100.0	226	1	PCT-US01-41430-21
4	1149	100.0	248	1	PCT-US01-06769-12
5	1149	100.0	288	1	PCT-US01-41430-15
6	1149	100.0	288	3	US-07-751-306C-2
7	1149	100.0	288	5	US-08-109-393A-29

8	1149	100.0	288	5	US-08-147-773-6	Sequence 6, Appl
9	1149	100.0	288	6	US-08-280-757-29	Sequence 29, Appl
10	1149	100.0	288	8	US-08-435-816A-2	Sequence 2, Appl
11	1149	100.0	288	8	US-08-453-386-2	Sequence 2, Appl
12	1149	100.0	288	8	US-08-453-386A-2	Sequence 2, Appl
13	1149	100.0	288	9	US-08-592-711-2	Sequence 2, Appl
14	1149	100.0	288	16	US-09-206-132-6	Sequence 6, Appl
15	1149	100.0	288	16	US-09-277-575-2	Sequence 2, Appl
16	1149	100.0	288	17	US-09-350-202-2	Sequence 2, Appl
17	1149	100.0	288	17	US-09-368-581-6	Sequence 6, Appl
18	1149	100.0	288	18	US-09-425-516-29	Sequence 29, Appl
19	1149	100.0	288	18	US-09-425-762-29	Sequence 29, Appl
20	1149	100.0	288	19	US-09-522-206-2	Sequence 2, Appl
21	1149	100.0	288	19	US-09-565-316A-2	Sequence 2, Appl
22	1149	100.0	288	20	US-09-620-461-5	Sequence 5, Appl
23	1149	100.0	288	20	US-09-651-200-13	Sequence 13, Appl
24	1149	100.0	288	20	US-09-667-135-34	Sequence 34, Appl
25	1149	100.0	288	21	US-09-711-022-2	Sequence 2, Appl
26	1149	100.0	288	21	US-09-716-928-2	Sequence 2, Appl
27	1149	100.0	288	21	US-09-716-928-8	Sequence 8, Appl
28	1149	100.0	288	21	US-09-772-102-14	Sequence 14, Appl
29	1149	100.0	288	22	US-09-837-867-19	Sequence 19, Appl
30	1149	100.0	288	22	US-09-868-605-1	Sequence 1, Appl
31	1149	100.0	288	22	US-09-896-738-10	Sequence 10, Appl
32	1149	100.0	288	23	US-09-910-174A-5	Sequence 5, Appl
33	1149	100.0	288	23	US-09-962-969-19	Sequence 19, Appl
34	1149	100.0	288	23	US-09-966-148-2	Sequence 2, Appl
35	1149	100.0	288	23	US-10-041-319-7	Sequence 7, Appl
36	1149	100.0	288	24	US-09-910-059-131	Sequence 131, App
37	1149	100.0	288	24	US-09-968-029-51	Sequence 51, Appl
38	1146	99.7	251	18	PCT-US97-12599-3	Sequence 3, Appl
39	1143	99.5	492	16	US-09-202-346-3	Sequence 3, Appl
40	1143	99.5	492	22	US-09-845-899A-3	Sequence 3, Appl
41	1143	99.5	492	22	US-09-845-899A-3	Sequence 3, Appl
42	1143	99.5	492	22	US-09-845-899A-3	Sequence 3, Appl
43	1142	99.4	288	3	US-07-591-300A-2	Sequence 2, Appl
44	1142	99.4	288	3	US-07-591-300A-2	Sequence 2, Appl
45	1138	99.0	480	18	US-09-468-029-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-459-766B-8
Sequence 8, Application US/08459766B
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Danle, Milin K.
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
FILE REFERENCE: 30436, 11US04
CURRENT APPLICATION NUMBER: US/08/459, 766B
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/498, 949
PRIOR FILING DATE: 1990-03-26
PRIOR APPLICATION NUMBER: 07/547, 980
PRIOR FILING DATE: 1990-07-02
PRIOR APPLICATION NUMBER: 07/722, 101
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 08/219, 200
PRIOR FILING DATE: 1994-03-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Freeman, Gordon J.
AUTHORS: Freeman, Arnold S.
AUTHORS: Segall, Jeffrey M.

;; AUTHORS: Lee, Grace
;; AUTHORS: Whitman, James F.
;; AUTHORS: Nadler, Lee M.
;; TITLE: B7, A NEW MEMBER OF THE IG SUPERFAMILY WITH UNIQUE
;; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
;; JOURNAL: J. Immunol.
;; VOLUME: 143
;; ISSUE: 8
;; PAGES: 2714-2722
;; DATE: 1989-10-15
;; RELEVANT RESIDUES: 1 TO 216
US-08-459-766B-8

Query Match 100.0%; Score 1149; DB 8; Length 216;
Best Local Similarity 100.0%; Pred. No. 6.4e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 60
DB 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 60
QY 61 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 120
DB 61 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 120
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180
DB 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180
QY 181 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 216
DB 181 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 216

RESULT 2
US-09-569-164A-8
; Sequence 8, Application US/09569164A
; GENERAL INFORMATION:
; APPLICANT: LINSLEY, PETER S. ET AL.
; TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/569,164A
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 07/547,980
; PRIOR FILING DATE: 1990-07-02
; PRIOR APPLICATION NUMBER: 07/722,101
; PRIOR FILING DATE: 1991-06-27
; PRIOR APPLICATION NUMBER: 08/219,200
; PRIOR FILING DATE: 1994-03-29
; PRIOR APPLICATION NUMBER: 08/459,766
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Freeman, Gordon J.
; AUTHORS: Freedman, Arnold S.
; AUTHORS: Segal, Jeffrey M.
; AUTHORS: Lee, Grace
; AUTHORS: Whitman, James F.
; AUTHORS: Nadler, Lee M.
; TITLE: B7, A NEW MEMBER OF THE IG SUPERFAMILY WITH UNIQUE
; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
; JOURNAL: J. Immunol.
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 1989-10-15
; RELEVANT RESIDUES: 1 TO 216

US-09-569-164A-8

Query Match 100.0%; Score 1149; DB 19; Length 216;
Best Local Similarity 100.0%; Pred. No. 6.4e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 60
DB 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 60
QY 61 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 120
DB 61 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 120
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180
DB 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180
QY 181 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 216
DB 181 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 216

RESULT 3
PCT-US01-41430-21
; Sequence 21, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-41430-21

Query Match 100.0%; Score 1149; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 6.8e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 60
DB 11 GLSHFCGVIHYTKVEKVAATLSCGHNVSEELAQTRITWQKEKKVLTMMSGDMNIWPE 70
QY 61 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 120
DB 71 YKRRITFDITNNLSIYIALRPSDEGTGECVYLKYEKDAFRKREHLAEVTLISKADFPPTS 130
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180
DB 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 190
QY 181 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 216
DB 191 NMTNHSFMCILIKYGLRVNQTENMTTKQEHPPDN 226

RESULT 4
PCT-US01-06769-12
; Sequence 12, Application PC/TUS0106769
; GENERAL INFORMATION:
; APPLICANT: Mayo Medical Ventures
; TITLE OF INVENTION: hB7-H2, A NOVEL CO-STIMULATORY MOLECULE
; FILE REFERENCE: 07039-202W01

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-07-751-306C-2

Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHFSGVIAHTVKEKVEATISCGHNVSVEELAOTRIYQWKKKAVLTMSGDMMIPE 60
DB 27 GSHFSGVIAHTVKEKVEATISCGHNVSVEELAOTRIYQWKKKAVLTMSGDMMIPE 86
QY 61 YKNRTIFDTNNLSIVIALRPSDEGTVECVVLKYEKDAFKREHLAEVTLSTVADFPPTPS 120

DB 87 YKNRTIFDTNNLSIVIALRPSDEGTVECVVLKYEKDAFKREHLAEVTLSTVADFPPTPS 146
QY 121 ISDEIPIPSNIRRIICSTGSGFPEPHLSWLENGELNAINFTVSQDPELEYAVSSKIDF 180
DB 147 ISDEIPIPSNIRRIICSTGSGFPEPHLSWLENGELNAINFTVSQDPELEYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHRLRVNQTFFMNTTKOEHFPDN 216
DB 207 NMTNHSFMCILIKYGHRLRVNQTFFMNTTKOEHFPDN 242
RESULT 7
US-08-109-393A-29
Sequence 29, Application US/08109393A
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,393A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:

NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-109-393A-29

Query Match 100.0%; Score 1149; DB 5; Length 288;

Best Local Similarity 100.0%; Pred. No. 9.7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFGSGVHVHTKEVEVATLSCGHNVSVBELAQRTIYWKKEKKMYLTMMSGDMNTIPE 60
Db 27 GLSHFGSGVHVHTKEVEVATLSCGHNVSVBELAQRTIYWKKEKKMYLTMMSGDMNTIPE 86
QY 61 YKNTIDITNNLSIVILALRPSDEGTGCVLKYEKDAFKREHLAEVTLVSKADPFTPS 120
Db 87 YKNTIDITNNLSIVILALRPSDEGTGCVLKYEKDAFKREHLAEVTLVSKADPFTPS 146
QY 121 ISDFEFTSNIRITCSTSGGPEPHLSMLENGEELNAINTVVSQDETELIVASSKLD 180
Db 147 ISDFEFTSNIRITCSTSGGPEPHLSMLENGEELNAINTVVSQDETELIVASSKLD 206
QY 181 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOHPDN 216
Db 207 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOHPDN 242

RESULT 8
US-08-147-773-6
; Sequence 6, Application US/08147773
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,773
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPT-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-147-773-6

Query Match 100.0%; Score 1149; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSGVHVHTKEVEVATLSCGHNVSVBELAQRTIYWKKEKKMYLTMMSGDMNTIPE 60
Db 27 GLSHFGSGVHVHTKEVEVATLSCGHNVSVBELAQRTIYWKKEKKMYLTMMSGDMNTIPE 86

Query Match 100.0%; Score 1149; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 9,7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVHYHVEKEVATLSCGHNVSEELAQTRIVQKCKKWLTMGSDMNIWPE 60
|||
DB 27 GLSHFCSGVHYHVEKEVATLSCGHNVSEELAQTRIVQKCKKWLTMGSDMNIWPE 86
|||
QY 61 YKRRTFDITNNSTIVTLARPSEDEGVECVLAKENDAKRREHLAVTISVKADEPTPS 120
|||
DB 87 YKRRTFDITNNSTIVTLARPSEDEGVECVLAKENDAKRREHLAVTISVKADEPTPS 146
|||
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPLSWLNGEELNNTVTSODETELYAVSSKIDF 180
|||
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPLSWLNGEELNNTVTSODETELYAVSSKIDF 206
|||
QY 181 NMTTNSFMCILYGHHRVNOTNNMTTKOEHPDN 216
|||
DB 207 NMTTNSFMCILYGHHRVNOTNNMTTKOEHPDN 242
|||

RESULT 10
US-08-435-816A-2
Sequence 2, Application US/08435816A
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennett, Paul D.
TITLE OF INVENTION: Methods for Selectively Stimulating Proliferation of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-435-816a-2

Query Match 100.0%; Score 1149; DB 8; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSIFCGVIVHTKEVEVATLSCGHNVSEBELAOTRIYWKKEKMYLTMSGDNIMPE 60
DB 27 GLSIFCGVIVHTKEVEVATLSCGHNVSEBELAOTRIYWKKEKMYLTMSGDNIMPE 86
DB 61 YKNTIFDITNNLSIVILALRPDSDEGYECVLYKYEKDAFKREHLAEVTLVSKADPPPS 120
DB 87 YKNTIFDITNNLSIVILALRPDSDEGYECVLYKYEKDAFKREHLAEVTLVSKADPPPS 146
QY 121 ISDEIFTSNRRITCSGGFPERHLSWLENGEELNAINTVSODPELELYAVSSKIDF 180
DB 147 ISDEIFTSNRRITCSGGFPERHLSWLENGEELNAINTVSODPELELYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGLHVRNQTFFMNTTKOEHFPDN 216
DB 207 NMTNHSFMCILIKYGLHVRNQTFFMNTTKOEHFPDN 242

RESULT 11
US-08-453-386-2
Sequence 2, Application US/08453386
GENERAL INFORMATION:
APPLICANT: FREEMAN, GORDON J.
APPLICANT: FREEDMAN, ARNOLD S.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: Of The Ig Superfamily With Unique Expression On
TITLE OF INVENTION: Activated And Neoplastic B Cells.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30

OPERATING SYSTEM: MS/DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,386
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
APPLICATION NUMBER: US 07/591,300
FILING DATE: 01-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:

```
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-453-386-2

Query Match      100.0%; Score 1149; DB 8; Length 288;
Best Local Similarity 100.0%; Pred. No. 9,7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEKVAATLSCGHNVSVBELAOTRIYWKKEKKVLTMMSGDMNIPE 60
DB 27 GLSHFCGVIHVTKEVEKVAATLSCGHNVSVBELAOTRIYWKKEKKVLTMMSGDMNIPE 86
QY 61 YKNTIFDITNNLSIVLLALRPSDEGTVECVLTKERDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNNLSIVLLALRPSDEGTVECVLTKERDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRIICSTSGGFPEPHLSMLENGEELNAINTVSQDPETELIYAVSKIDF 180
DB 147 ISDFEIPTSNIRIICSTSGGFPEPHLSMLENGEELNAINTVSQDPETELIYAVSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOEHPDN 242

RESULT 12
US-08-453-386A-2
; Sequence 2, Application US/08453386A
; GENERAL INFORMATION:
; APPLICANT: FREEDMAN, Gordon J.
; APPLICANT: FREEDMAN, Arnold S.
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: DNA Encoding B7, A New Member Of The IgG Superfamily
; TITLE OF INVENTION: With Unique Expression On Activated And Neoplastic B
; TITLE OF INVENTION: Cells
```

```
FILE REFERENCE: RPI-01ACNDV
CURRENT APPLICATION NUMBER: US/08/453,386A
CURRENT FILING DATE: 1995-05-30
PRIOR APPLICATION NUMBER: 08/153,262
PRIOR FILING DATE: 1993-11-15
PRIOR APPLICATION NUMBER: 07/751,306
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: 07/591,300
PRIOR FILING DATE: 1990-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 288
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (35)
NAME/KEY: DOMAIN
LOCATION: (1)..(208)
NAME/KEY: TRANSMEM
LOCATION: (209)..(235)
NAME/KEY: DOMAIN
LOCATION: (236)..(254)
OTHER INFORMATION: Intracellular
OTHER INFORMATION: N-linked glycosylation at position 19 to 21
OTHER INFORMATION: N-linked glycosylation at position 55 to 57
OTHER INFORMATION: N-linked glycosylation at position 64 to 66
OTHER INFORMATION: N-linked glycosylation at position 152 to 154
OTHER INFORMATION: N-linked glycosylation at position 173 to 175
OTHER INFORMATION: N-linked glycosylation at position 177 to 179
OTHER INFORMATION: N-linked glycosylation at position 192 to 194
OTHER INFORMATION: N-linked glycosylation at position 198 to 200
NAME/KEY: DOMAIN
LOCATION: (1)..(104)
OTHER INFORMATION: Ig V-set
NAME/KEY: DOMAIN
LOCATION: (105)..(202)
OTHER INFORMATION: Ig C-set
OTHER INFORMATION: Description of Artificial Sequence: Primer
OTHER INFORMATION: Signal sequence from positions -34 through -1
JOURNAL: J. Immunol.
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
US-08-453-386A-2

Query Match      100.0%; Score 1149; DB 8; Length 288;
Best Local Similarity 100.0%; Pred. No. 9,7e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEKVAATLSCGHNVSVBELAOTRIYWKKEKKVLTMMSGDMNIPE 60
DB 27 GLSHFCGVIHVTKEVEKVAATLSCGHNVSVBELAOTRIYWKKEKKVLTMMSGDMNIPE 86
QY 61 YKNTIFDITNNLSIVLLALRPSDEGTVECVLTKERDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNNLSIVLLALRPSDEGTVECVLTKERDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRIICSTSGGFPEPHLSMLENGEELNAINTVSQDPETELIYAVSKIDF 180
DB 147 ISDFEIPTSNIRIICSTSGGFPEPHLSMLENGEELNAINTVSQDPETELIYAVSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNOTFMNNTTKOEHPDN 242

RESULT 13
```

US-08-592-711-2
Sequence 2, Application US/08592711
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Renner, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
NAME/KEY: extracellular domain

LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology

: VOLUME: 143
 : ISSUE: 8
 : PAGES: 2714-2722
 : DATE: 15-OCT-1989
 : RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 :
 : US-08-592-711-2

Query Match	100.0%	Score 1149;	DB 9;	Length 288;
Best Local Similarity	100.0%	Pred. No. 9.7e-112;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	1	GLSHHSCGVIVHYTEKVKVAVLSCGHNVSVBELAOTRIYWKKEKRVLTJMSGMINIPE	60
Db	27	GLSHHSCGVIVHYTEKVKVAVLSCGHNVSVBELAOTRIYWKKEKRVLTJMSGMINIPE	86
Oy	61	YKNRTIFDITNNLSIVIALRPSDEGIVTECVULYKDKAEKREHLAEVTLISVKADPPTPS	120
Db	87	YKNRTIFDITNNLSIVIALRPSDEGIVTECVULYKDKAEKREHLAEVTLISVKADPPTPS	146
Oy	121	ISDFEIPISNRIIRICISGSGFPEPHITSMLENGEELNAINTVSODPETELIYAASSKIDF	180
Db	147	ISDFEIPISNRIIRICISGSGFPEPHITSMLENGEELNAINTVSODPETELIYAASSKIDF	206
Oy	181	NMTTNHSFMCILIKYUHLRVNQTGMNNTTKOEHPFDN	216
Db	207	NMTTNHSFMCILIKYUHLRVNQTGMNNTTKOEHPFDN	242

```

1 RESULT 14
2 US-09-206-132-6
3 ; Sequence 6, Application US/09206132
4 ;
5 ; GENERAL INFORMATION:
6 ;
7 ; APPLICANT: Freeman, Gordon J.
8 ;
9 ; APPLICANT: Nadler, Lee M.
10 ;
11 ; APPLICANT: Gray, Gary S.
12 ;
13 ; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
14 ;
15 ; TITLE OF INVENTION: WITH INCREASED IMMUNOGENICITY AND USES THEREFOR
16 ;
17 ; NUMBER OF SEQUENCES: 8
18 ;
19 ; CORRESPONDENCE ADDRESS:
20 ;
21 ; ADDRESSEE: LAHIVE & COCKFIELD
22 ;
23 ; STREET: 60 State Street, Suite 510
24 ;
25 ; CITY: Boston
26 ;
27 ; STATE: Massachusetts
28 ;
29 ; COUNTRY: USA
30 ;
31 ; ZIP: 02109
32 ;
33 ; COMPUTER READABLE FORM:
34 ;
35 ; MEDIUM TYPE: Floppy disk
36 ;
37 ; COMPUTER: IBM PC compatible
38 ;
39 ; OPERATING SYSTEM: PC-DOS/MS-DOS
40 ;
41 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
42 ;
43 ; CURRENT APPLICATION DATA:
44 ;
45 ; APPLICATION NUMBER: US/09/206,132
46 ;
47 ; FILING DATE:
48 ;
49 ; CLASSIFICATION:
50 ;
51 ; PRIORITY APPLICATION DATA:
52 ;
53 ; APPLICATION NUMBER: 08/456,104
54 ;
55 ; FILING DATE:
56 ;
57 ; APPLICATION NUMBER: 08/101,624
58 ;
59 ; FILING DATE: 26-JUL-1993
60 ;
61 ; APPLICATION NUMBER: 08/109,393
62 ;
63 ; APPLICATION NUMBER: 19-AUG-1993
64 ;
65 ; ATTORNEY/AGENT INFORMATION:
66 ;
67 ; NAME: Mandragouras, Amy E.
68 ;
69 ; REGISTRATION NUMBER: 36,207
70 ;
71 ; REFERENCE/DOCKET NUMBER: RPT-008
72 ;
73 ; TELECOMMUNICATION INFORMATION:
74 ;
75 ; TELEPHONE: (617) 227-7400
76 ;
77 ; TELEFAX: (617) 227-5941
78 ;
79 ; INFORMATION FOR SEQ ID NO: 6:
80 ;
81 ; SEQUENCE CHARACTERISTICS:
82 ;
83 ; LENGTH: 288 amino acids
84 ;
85 ; TYPE: amino acid
86 ;
87 ;
88 ;
89 ;
90 ;
91 ;
92 ;
93 ;
94 ;
95 ;
96 ;
97 ;
98 ;
99 ;

```

```

;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-206-132-6

```

Query Match	100.0%;	Score 1149;	DB 16;	Length 288;
Best Local Similarity	100.0%;	Pred. No. 9.7e-112;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GLSHCCSCVIAHTEVEKEVALSCGHNVSEBELAQOTIYQKKEKMYLTMSGDMMIWE	60
Db	27	GLSHCCSCVIAHTEVEKEVALSCGHNVSEBELAQOTIYQKKEKMYLTMSGDMMIWE	86
Qy	61	YKNRTIEDIINNLSVIALRPPDEGVEYECVLYEKDAREHLAEVLTSVKADPPTPS	120
Db	87	YKNRTIEDIINNLSVIALRPPDEGVEYECVLYEKDAREHLAEVLTSVKADPPTPS	146
Qy	121	ISDFEIPISNRIICSTSGGEPBPHLSWLENGELNAINTVSODEPTELAVSSKLD	180
Db	147	ISDFEIPISNRIICSTSGGEPBPHLSWLENGELNAINTVSODEPTELAVSSKLD	206
Qy	181	NMTTNSHSPCLIKYGHLELVNQTGMNTTCKQEHFND	216
Db	207	NMTTNSHSPCLIKYGHLELVNQTGMNTTCKQEHFND	242

```

RESULT 15
US-09-277-575-2
; Sequence 2: Application US/09277575
;
; GENERAL INFORMATION:
;
; APPLICANT: Newell, Martha K
;
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR
; METABOLIC INTERACTIONS
;
; FILE REFERENCE: VO133/7028/HK
;
; CURRENT APPLICATION NUMBER: US/09/277,575
;
; CURRENT FILING DATE: 1999-03-26
;
; EARLIER APPLICATION NUMBER: U.S. 60/082,250
;
; EARLIER FILING DATE: 1998-04-17
;
; EARLIER APPLICATION NUMBER: U.S. 60/094,519
;
; EARLIER FILING DATE: 1998-07-29
;
; EARLIER APPLICATION NUMBER: U.S. 60/101,580
;
; EARLIER FILING DATE: 1998-09-24
;
; NUMBER OF SEQ ID NOS: 13
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 2
;
; LENGTH: 288
;
; TYPE: prt
;
; ORGANISM: Homo Sapiens
;
US-09-277-575-2

```

Query Match	100.0%;	Score 1149;	DB 16;	Length 288;
Best Local Similarity	100.0%;	Pred. No. 9.7e-112;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GSHHCOSGVIHNTKKVKKEVATLSCGHNVSVBELQOTRIYMOKEKKMYLTMMSGDMNTMPE	60
Db	27	GISHHCSGVIHNTKKVKKEVATLSCGHNVSVBELQOTRIYMOKEKKMYLTMMSGDMNTMPE	86
QY	61	YKNRTIFDTNNMLSTVILLALRPSDGTCEVCVLLYKEDAFKREHLAEVTLISVKADPEPTPS	120
Db	87	YKNRTIFDTNNMLSTVILLALRPSDGTCEVCVLLYKEDAFKREHLAEVTLISVKADPEPTPS	146
QY	121	ISDFEIPISNIRRICSTSGGPPPEHLSWLMGEBELNAINTVSQDEPTELYAVSSKIDF	180
Db	147	ISDFEIPISNIRRICSTSGGPPPEHLSWLMGEBELNAINTVSQDEPTELYAVSSKIDF	206
QY	181	NMTNHSFMCILKYGHLRNVQFENMNTKOEHPFN	216
Db	207	NMTNHSFMCILKYGHLRNVQFENMNTKOEHPFN	242

Tue Jun 18 11:51:12 2002

us-09-454-651b-23.rapm

Page 12

Search completed: June 18, 2002, 11:46:50
Job time: 223 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 11:43:07 ; Search time 13.09 Seconds
(without alignments)
403.050 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVHVTKEKEVA.....LRVNFENMTTKQEHFEDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	2	US-08-147-772-2
2	1149	100.0	288	2	US-08-456-104-6
3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	2	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-479-744A-29
7	1149	100.0	288	4	US-08-280-757B-29
8	1149	100.0	288	4	US-09-159-135-2
9	1149	100.0	288	4	US-08-205-697A-19
10	1149	100.0	288	4	US-08-702-525-19
11	1149	100.0	288	4	US-09-450-798-2
12	1149	100.0	288	4	US-08-403-253A-2
13	1149	100.0	288	5	PCT-US95-02576-19
14	1149	100.0	473	4	US-09-171-945-131
15	1102	95.9	208	4	US-09-460-384-36
16	1050	91.4	208	3	US-08-630-172-15
17	1050	91.4	208	4	US-09-375-419-15
18	561	48.8	306	4	US-08-205-697A-17
19	561	48.8	306	4	US-08-702-525-17
20	561	48.8	306	5	PCT-US95-02576-17
21	561	48.8	320	4	US-08-205-697A-2
22	561	48.8	320	4	US-08-702-525-2
23	561	48.8	320	5	PCT-US95-02576-2
24	558	48.6	306	2	US-08-147-772-4
25	558	48.6	306	2	US-08-456-104-8
26	558	48.6	306	2	US-08-101-624-25
27	558	48.6	306	3	US-08-153-262-4

28	558	48.6	306	3	US-08-479-744A-31	Sequence 31, Appl
29	558	48.6	306	4	US-08-280-757B-31	Sequence 31, Appl
30	558	48.6	306	4	US-09-159-135-4	Sequence 4, Appl
31	558	48.6	306	4	US-09-450-798-4	Sequence 4, Appl
32	311	27.1	200	4	US-08-205-697A-9	Sequence 9, Appl
33	311	27.1	200	4	US-08-702-525-9	Sequence 9, Appl
34	311	27.1	200	5	PCT-US95-02576-9	Sequence 9, Appl
35	311	27.1	214	4	US-08-205-697A-11	Sequence 11, Appl
36	311	27.1	214	4	US-08-702-525-11	Sequence 11, Appl
37	311	27.1	214	5	PCT-US95-02576-11	Sequence 11, Appl
38	250.5	21.8	212	4	US-08-702-525-63	Sequence 63, Appl
39	250.5	21.8	212	5	PCT-US95-02576-63	Sequence 63, Appl
40	250.5	21.8	226	4	US-08-702-525-65	Sequence 65, Appl
41	250.5	21.8	226	5	PCT-US95-02576-65	Sequence 65, Appl
42	182	15.8	323	5	PCT-US94-09642-2	Sequence 2, Appl
43	182	15.8	329	2	US-08-456-104-2	Sequence 2, Appl
44	182	15.8	329	2	US-08-101-624-2	Sequence 2, Appl
45	182	15.8	329	3	US-08-479-744A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,772
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of

```

? IDENTIFICATION METHOD: soluble protein
? OTHER INFORMATION: hydrophobic
? FEATURE:
? NAME/KEY: extracellular domain
? LOCATION: 1 to 208
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: transmembrane domain
? LOCATION: 209 to 235
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: intracellular domain
? LOCATION: 236 to 254
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 19 to 21
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 55 to 57
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 64 to 66
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 152 to 154
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 173 to 175
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 177 to 179
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 192 to 194
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: N-linked glycosylation
? LOCATION: 198 to 200
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: Ig V-set domain
? LOCATION: 1 to 104
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? FEATURE:
? NAME/KEY: Ig C-set domain
? LOCATION: 105 to 202
? IDENTIFICATION METHOD: similarity with known
? IDENTIFICATION METHOD: sequence
? PUBLICATION INFORMATION:
? AUTHORS: FREEMAN, GORDON J.
? AUTHORS: FREEDMAN, ARNOLD S.
? AUTHORS: SEGIL, JEFFREY M.
? AUTHORS: LEE, GRACE
? AUTHORS: WHITMAN, JAMES F.

```

```

? AUTHORS: NADLER, LEE M.
? TITLE: B7, A New Member Of The Ig Superfamily With
? TITLE: Unique Expression On Activated And Neoplastic B Cells
? JOURNAL: The Journal of Immunology
? VOLUME: 143
? ISSUE: 8
? PAGES: 2714-2722
? DATE: 15-OCT-1989
? RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2

```

```

Query Match          100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5,2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GISHFCGVIHVTKEKEVATLSCGHNVSEELAQRIYWEKKKMYLTMMSGDMNIWPE 60
DB 27 GISHFCGVIHVTKEKEVATLSCGHNVSEELAQRIYWEKKKMYLTMMSGDMNIWPE 86
QY 61 YKNRTIPITNNLSIVILALRPSDEGTVCYVLYKFKDAFKRHLAEVTLVSKADPTPS 120
DB 87 YKNRTIPITNNLSIVILALRPSDEGTVCYVLYKFKDAFKRHLAEVTLVSKADPTPS 146
QY 121 ISDEPIPTSNIRIICSTSGCFPEPHLSWLNGEELNAINTVSODPELTVSSKLPD 180
DB 147 ISDEPIPTSNIRIICSTSGCFPEPHLSWLNGEELNAINTVSODPELTVSSKLPD 206
QY 181 NMTNHSFMCILIKYGLRNVQTFNNMTTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGLRNVQTFNNMTTKOEHPDN 242

```

```

RESULT 2
US-08-456-104-6
? Sequence 6, Application US/08456104
? Patent No. 5861310
? GENERAL INFORMATION:
? APPLICANT: Freeman, Gordon J.
? APPLICANT: Nadler, Lee M.
? APPLICANT: Gray, Gary S.
? TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 State Street, Suite 510
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/456,104
? FILING DATE:
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/101,624;
? FILING DATE: 26-JUL-1993;
? APPLICATION NUMBER: 08/109,393;
? APPLICATION NUMBER: 19-AUG-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragouras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: RPI-008
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 227-7400
? TELEFAX: (617) 227-5941
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:

```

LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-6

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5,2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFSGVHYHKEKREKVAATLSCGHNVSYEEIAQRIYQKQKRWLTMMSGDMNTWPE 60
|||||
DB 27 GLSHFSGVHYHKEKREKVAATLSCGHNVSYEEIAQRIYQKQKRWLTMMSGDMNTWPE 86
|||||

QY 61 YKRRITFDITNNISYILALRPSDEGTGECVVLKYEKDAKREHLAEVTLVKADEPTPS 120
|||||
DB 87 YKRRITFDITNNISYILALRPSDEGTGECVVLKYEKDAKREHLAEVTLVKADEPTPS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLNGBELNAINTVSODETELAVVSSKLD 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLNGBELNAINTVSODETELAVVSSKLD 206
|||||

QY 181 NMTNHSFMCILIKYGHRLVNOTFNMTTKQEHPPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLVNOTFNMTTKQEHPPDN 242
|||||

RESULT 3
US-08-101-624-23
Sequence 23, Application US/08101624
Patent No. 5942607

GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic

FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.

AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 13-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
US-08-101-624-23

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFSGVIVHTKEVEKAVATLSCGHNVSYELAQTRITYMOKKKMVLTMMSGDMNIMPE 60
DB 27 GLSHFSGVIVHTKEVEKAVATLSCGHNVSYELAQTRITYMOKKKMVLTMMSGDMNIMPE 86
QY 61 YKRRITFDITNNISIVILALRPSDEGTVECVLYKEKDAKREHLAEVTLVSKADPTPPS 120
DB 87 YKRRITFDITNNISIVILALRPSDEGTVECVLYKEKDAKREHLAEVTLVSKADPTPPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVTSQDPETELIYAVSSKIDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVTSQDPETELIYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFNMNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFNMNTTKQEHFPDN 242

RESULT 4

US-08-751-767A-6
Sequence 6, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLEUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-751-767A-6

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFSGVIVHTKEVEKAVATLSCGHNVSYELAQTRITYMOKKKMVLTMMSGDMNIMPE 60
DB 27 GLSHFSGVIVHTKEVEKAVATLSCGHNVSYELAQTRITYMOKKKMVLTMMSGDMNIMPE 86
QY 61 YKRRITFDITNNISIVILALRPSDEGTVECVLYKEKDAKREHLAEVTLVSKADPTPPS 120
DB 87 YKRRITFDITNNISIVILALRPSDEGTVECVLYKEKDAKREHLAEVTLVSKADPTPPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVTSQDPETELIYAVSSKIDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVTSQDPETELIYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFNMNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFNMNTTKQEHFPDN 242

RESULT 5

US-08-153-262-2
Sequence 2, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
APPLICANT: FREEDMAN, GORDON J.
APPLICANT: FREEDMAN, ARNOLD S.
APPLICANT: NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: Of The Ig Superfamily With Unique Expression On
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.

AUTHORS: FREEMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2
Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No.5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFGSGVHIVTKEVEVATLSCGHNVSELAQTRITYMOKKKVLTMMSGDMNTIME 60
|||||
DB 27 GLSHFGSGVHIVTKEVEVATLSCGHNVSELAQTRITYMOKKKVLTMMSGDMNTIME 86
QY 61 YKNRTIDITNNLSIVILALRPDSDEGYECVYLKYEKDAFKREHLAEVTLVSKADPTPS 120
|||||
DB 87 YKNRTIDITNNLSIVILALRPDSDEGYECVYLKYEKDAFKREHLAEVTLVSKADPTPS 146
QY 121 ISDEIFPSNRIICSTSGSFPPEPHLSWLENGELNAINTVSODPETELVAVSSKIDF 180
|||||
DB 147 ISDEIFPSNRIICSTSGSFPPEPHLSWLENGELNAINTVSODPETELVAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHRLRVNQTENMNTTKOEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLRVNQTENMNTTKOEHFPDN 242
RESULT 6
US-08-479-744A-29
; Sequence 29, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE: for CD28 T cell surface antigen; transmembrane protein
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-479-744A-29

Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 5,2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHSCGYIHTYKKEKATLSGCHNVSEBELAQRIYQKKKAVLTMSGDNIWPE 60
|||||
DB 27 GLSHSCGYIHTYKKEKATLSGCHNVSEBELAQRIYQKKKAVLTMSGDNIWPE 86
61 YKRRIFDITNNLSYIILALRPSDEGTVCYVLYKYEKDAFKRHLAEVTLVSKADPTPS 120
|||||
DB 87 YKRRIFDITNNLSYIILALRPSDEGTVCYVLYKYEKDAFKRHLAEVTLVSKADPTPS 146
147 ISDFEIPISNIRIICSTSGCFPEPHLSWLENGEELNAINITVSDPELELVSSKIDF 206
QY 121 ISDFEIPISNIRIICSTSGCFPEPHLSWLENGEELNAINITVSDPELELVSSKIDF 180
|||||
DB 147 ISDFEIPISNIRIICSTSGCFPEPHLSWLENGEELNAINITVSDPELELVSSKIDF 206
QY 181 NMTNHSFMCILIKYGLRYNOTFNMTTKOEHPDN 216
|||||
DB 207 NMTNHSFMCILIKYGLRYNOTFNMTTKOEHPDN 242

RESULT 7
US-08-280-757B-29
Sequence 29, Application US/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/280,757B
APPLICATION NUMBER: 26-JUL-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
NAME/KEY: signal sequence
LOCATION: 34 to 41
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-280-757B-29
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTREKEVATLSGHNVSVEELAOTRIYOKKKKVLFMMSGDMNINPE 60
DB 27 GLSHFCSGVHVTREKEVATLSGHNVSVEELAOTRIYOKKKKVLFMMSGDMNINPE 86
QY 61 YKRNTPIDITNNLSIVLALRPSDEGTVECVLYKYKDAFKRHLAEVTLVYKADFPSP 120
DB 87 YKRNTPIDITNNLSIVLALRPSDEGTVECVLYKYKDAFKRHLAEVTLVYKADFPSP 146
QY 121 ISDEIPTSNIRRICTSGGFPPEPHLSWLENGEELNATITVSODPEELVAVSSKLP 180
DB 147 ISDEIPTSNIRRICTSGGFPPEPHLSWLENGEELNATITVSODPEELVAVSSKLP 206
QY 181 NMTNHSFMCILIKYGHLRVNOTFWMNTTKOEHFPDN 216
DB 207 NMTNHSFMCILIKYGHLRVNOTFWMNTTKOEHFPDN 242
RESULT 8
US-09-159-135-2
Sequence 2, Application US/09159135
Patent No. 6149905
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells with Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
FAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 153 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-159-135-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5,2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFGCVIHVTEKEVEATVLSGHNYSVELAOTRIYMOKEKMYITMMSGDMNTPE 60
Db 27 GLSHFGCVIHVTEKEVEATVLSGHNYSVELAOTRIYMOKEKMYITMMSGDMNTPE 86
QY 61 YKNTIFDITNNLSIVIALRPDSDEGYECVILKYERDAFREHLAEVTLISVKADFPPTS 120
Db 87 YKNTIFDITNNLSIVIALRPDSDEGYECVILKYERDAFREHLAEVTLISVKADFPPTS 146
QY 121 ISDEIFPTSNRRITGSGGPEPHLSWLENGEELNAINTVSODEPTELIAVSSKIDF 180
Db 147 ISDEIFPTSNRRITGSGGPEPHLSWLENGEELNAINTVSODEPTELIAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGLRVNQTENMNTTKOEHPPDN 216

Db 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 9

US-08-205-697A-19

; Sequence 19, Application US/08205697A

; Patent No. 6218510

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Arlene H.

; APPLICANT: Borriello, Francescopaulo

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules

; NUMBER OF SEQUENCES: 61

; TITLE OF INVENTION: and Uses Therefor

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/205,697A

; FILING DATE: 02-Mar-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: BWI-120

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 288 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-205-697A-19

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVYIHTYKREKAVATLSCGHNVSEELAQTRITYWQEKKKVLTMSGDMNIMPE 60
Db 27 GLSHFCGVYIHTYKREKAVATLSCGHNVSEELAQTRITYWQEKKKVLTMSGDMNIMPE 86
QY 61 YKNRTIFDITNNLSIVIALRPSDEGTGYCVLYKYEKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVIALRPSDEGTGYCVLYKYEKDAFKREHLAEVTLVSKADFPPTS 146
QY 121 ISDFEIPSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELAVASSKIDF 180
Db 147 ISDFEIPSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELAVASSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216
Db 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 10

US-08-702-525-19

; Sequence 19, Application US/08702525

; Patent No. 6294660

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Sharpe

; APPLICANT: Borriello, Francescopaulo

; APPLICANT: Freeman, Gordon

; APPLICANT: Nadler, Lee

; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory

; NUMBER OF SEQUENCES: 65

; TITLE OF INVENTION: Molecules and Uses Therefor

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/702,525

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/205,697

; FILING DATE: 02-Mar-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: BWI-120CPUS

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 288 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-702-525-19

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVYIHTYKREKAVATLSCGHNVSEELAQTRITYWQEKKKVLTMSGDMNIMPE 60
Db 27 GLSHFCGVYIHTYKREKAVATLSCGHNVSEELAQTRITYWQEKKKVLTMSGDMNIMPE 86
QY 61 YKNRTIFDITNNLSIVIALRPSDEGTGYCVLYKYEKDAFKREHLAEVTLVSKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVIALRPSDEGTGYCVLYKYEKDAFKREHLAEVTLVSKADFPPTS 146
QY 121 ISDFEIPSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELAVASSKIDF 180
Db 147 ISDFEIPSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELAVASSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216
Db 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 11

US-09-450-798-2

; Sequence 2, Application US/09450798

; Patent No. 6319709

; GENERAL INFORMATION:

; APPLICANT: Ostrand-Rosenberg, Suzanne

; APPLICANT: Baskar, Sivasubramanian

; APPLICANT: Glimcher, Laurie H.

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity

; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/450,798
FILING DATE: 29-NOV-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-450-798-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHFCSGVIVHTKEKEVAATLSCGHNVSEELAQRIYQKEKKVLTMMSGDMNTPE 60
DB 27 GSHFCSGVIVHTKEKEVAATLSCGHNVSEELAQRIYQKEKKVLTMMSGDMNTPE 86
QY 61 YKRRITFDITNNLSIVTLARPSDEGTVECVLKYEDARKREHLAVTYSVKADFPSP 120
DB 87 YKRRITFDITNNLSIVTLARPSDEGTVECVLKYEDARKREHLAVTYSVKADFPSP 146
QY 121 ISDFEIPTSNIRRICSTSGGFEPHLSWLENGEELNAINTTVSQDETELYAVSKLDF 180
DB 147 ISDFEIPTSNIRRICSTSGGFEPHLSWLENGEELNAINTTVSQDETELYAVSKLDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTENMNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTENMNTTKQEHFPDN 242
RESULT 12
US-08-403-253A-2
; Sequence 2, Application US/08403253A

Patent No. 6352694
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
FEATURE: signal sequence
LOCATION: 34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal Of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-403-253A-2

PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
SAME

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,384
FILING DATE: 13-Dec-1999

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12312
FILING DATE: 11-JUN-1998
APPLICATION NUMBER: US 60/049,470
FILING DATE: 12-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-460-384-36

Query Match 95.9%; Score 1102; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.8e-108;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	9	VIVHVKVEKVAATLSCGHNVSYELAQTRIVYQKQKQVLTMMSGDMIMPEYKKNRTFD	68
Db	1	VIVHVKVEKVAATLSCGHNVSYELAQTRIVYQKQKQVLTMMSGDMIMPEYKKNRTFD	60
Qy	69	ITNNLSIYIALRPSDEGTTECVLKYEKDAFKREHLAEVTLVSKADFPPTPSISDFEIPT	128
Db	61	ITNNLSIYIALRPSDEGTTECVLKYEKDAFKREHLAEVTLVSKADFPPTPSISDFEIPT	120
Qy	129	SNIRRICTSGGPEPHSWLNGEELNATITVSQDETELIVAVSSKLDNMTNHSF	188
Db	121	SNIRRICTSGGPEPHSWLNGEELNATITVSQDETELIVAVSSKLDNMTNHSF	180
Qy	189	MCLIKYGHILRVNQTFFNMNTTKQEHFPDN	216
Db	181	MCLIKYGHILRVNQTFFNMNTTKQEHFPDN	208

Search completed: June 18, 2002, 11:43:29
Job time: 22 sec

